SEQUENCE LISTING

<110>   Elich, Tedd D.
        Volrath, Sandra L.
        Weatherly, Stephanie C.

<120>   RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
        ACETYL CoA CARBOXYLASE INHIBITORS

<130>   9280.2

<150>   US 60/401,170
<151>   2003-08-05

<160>   71

<170>   PatentIn version 3.2

<210>   1
<211>   1677
<212>   DNA
<213>   Ustilago maydis

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1   5   10   15

ctt gaa acc gct ccc gcc agc cct gtt gcc gac ttt att cgc aaa cag   96
Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln
            20   25   30

ggt ggt cac agt gtc atc acc aag gtc ctc att tgc aac aac ggt atc   144
Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile
        35   40   45

gcc gcc gtc aag gag att cgc tcc atc cga aaa tgg gcc tac gag acc   192
Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr
    50   55   60

ttt ggc gat gag cgt gcc att gaa ttt acc gtc atg gcc acc cct gag   240
Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu
65   70   75   80

gac ctc aaa gtc aat gcc gac tac atc cgc atg gcc gac caa tac gtc   288
Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val
                85   90   95

gag gta ccc ggt ggc tct aac aac aac aac tac gct aac gtc gac ctc   336
Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu
            100   105   110

atc gtc gat gtc gct gag cga gcc ggc gtt cac gcc gta tgg gct ggc   384
Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly
        115   120   125

1

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tgg ggt cac gcc tcc gag aac cca cgc cta cct gaa tcg ctc gcc gcc          432
Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala
    130                     135                 140

tcc aag cac aag atc atc ttt atc ggt ccc ccc ggc tcc gcc atg cgc          480
Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg
145                     150                 155                 160

tcg ctt ggt gac aag atc tcg tcc acc atc gtc gca cag cac gcc gac          528
Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp
                165                 170                 175

gtg cca tgc atg ccc tgg tcc ggt acc ggc atc aag gag acc atg atg          576
Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met
            180                 185                 190

agc gat cag ggt ttc ctg acc gtc tcg gac gac gtc tac caa cag gcc          624
Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala
        195                 200                 205

tgc atc cac acc gct gaa gaa ggt ctt gag aag gcc gaa aag atc ggc          672
Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly
    210                     215                 220

tac ccc gtc atg atc aag gcc tcc gaa ggt gga gga gga aag ggt atc          720
Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
225                     230                 235                 240

cga aag tgt acc aac ggc gaa gaa ttc aag cag ctc tac aac gcc gtt          768
Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val
                245                 250                 255

ctc ggt gaa gtg ccc ggc tcg ccc gtt ttc gtt atg aaa ctc gcc ggc          816
Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly
                260                 265                 270

cag gcg cgt cat ctc gag gtg cag ctg ctg gcc gat cag tac ggc aac          864
Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn
            275                 280                 285

gcc atc agc atc ttt ggt cgt gac tgc tct gtc cag cgt cgt cac caa          912
Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
        290                 295                 300

aag atc atc gag gag gct cct gtc act atc gct cct gag gat gcc cgc          960
Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg
305                     310                 315                 320

gag tcc atg gag aag gct gcc gtg cgt ctc gcc aaa ctg gtt ggc tac        1008
Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr
                325                 330                 335

gtc tct gcc ggt acc gtc gaa tgg ctc tac tct ccc gag tcg ggc gag       1056
Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu
            340                 345                 350

ttt gcc ttc ctc gag ctc aac ccc cgt ctt cag gtc gag cac cct act       1104
Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
        355                 360                 365
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2

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acc gag atg gtc tcg ggt gtc aac att ccc gct gcc cag ctt cag gtc      1152
Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val
    370             375             380

gcc atg ggt atc cct ctc tac tcg atc cgc gac atc cga acc ctt tac      1200
Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr
385             390             395                 400

ggc atg gac cct cgc ggt aat gag gtc atc gac ttt gac ttc tct agc      1248
Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser
            405             410                 415

ccc gag tcg ttc aag acc cag cgc aag cct cag ccc cag ggc cac gta      1296
Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val
            420             425             430

gtc gcc tgc cgt atc act gcc gaa aac ccc gac acc ggc ttc aag cct      1344
Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro
            435             440             445

ggc atg ggt gcc ctc act gag ctc aac ttc cgc tcc agc acc tcc acc      1392
Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr
    450             455             460

tgg ggt tac ttc tcc gtc ggc acc agc ggt gct ctc cac gag tac gcc      1440
Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala
465             470             475             480

gat tcg cag ttc gga cac atc ttt gcc tat ggt gcc gac cga tcc gag      1488
Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu
            485             490             495

gcg cga aaa cag atg gtc atc tcg ctc aag gag ctc tcc att cgc ggt      1536
Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly
            500             505             510

gac ttc cgt acc acc gtc gaa tac ctc atc aag ttg ctc gag acc gac      1584
Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp
            515             520             525

gcc ttc gag tcc aac aag atc acc act gga tgg ctc gat ggt ctc att      1632
Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile
    530             535             540

cag gac cgt ctc act gcc gaa cga cct cct gcg gac ctc gct gtc          1677
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545             550             555
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<210> 2
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<212> PRT
<213> Ustilago maydis

<400> 2

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Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln
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3

Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile
        35   40   45

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr
        50   55   60

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu
65   70   75   80

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val
                85   90   95

Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu
            100   105   110

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly
            115   120   125

Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala
        130   135   140

Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg
145   150   155   160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp
                165   170   175

Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met
            180   185   190

Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala
            195   200   205

Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly
            210   215   220

Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
225   230   235   240

Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val
                245   250   255

Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly
            260   265   270

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Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn
        275             280             285

Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
        290             295             300

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg
305             310             315             320

Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr
            325             330             335

Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu
            340             345             350

Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
        355             360             365

Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val
    370             375             380

Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr
385             390             395             400

Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser
            405             410             415

Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val
            420             425             430

Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro
        435             440             445

Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr
    450             455             460

Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala
465             470             475             480

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu
            485             490             495

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly
            500             505             510
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5

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Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp
        515             520             525

Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile
        530             535             540

Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro Ala Asp Leu Ala Val
545             550             555
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<210> 3
<211> 1665
<212> DNA
<213> Phytophthora infestans

<220>
<221> CDS
<222> (1)..(1665)
<223> ACCase BC domain (aa 1-555)

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1               5               10              15

gag acg cgc agc gac agc aac ccg ctg aac tac gcg agc atg gag gag      96
Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu
            20              25              30

tat gtg cgt ctg cag aag ggt acg cgc ccc att acg tcc gtt ctg atc     144
Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile
            35              40              45

gcc aac aac ggt atc tcg gcc gtc aag gcc atc cgc agc atc cgc agc     192
Ala Asn Asn Gly Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser
    50              55              60

tgg agc tac gag atg ttc gct gac gaa cac gtc gtg acc ttc gtc gtc     240
Trp Ser Tyr Glu Met Phe Ala Asp Glu His Val Val Thr Phe Val Val
65              70              75              80

atg gct acg ccc gag gat ctt aag gct aat gca gag tac att cgc atg     288
Met Ala Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met
            85              90              95

gcc gaa cac gtc gtc gaa gtg ccc ggc ggc tcc aac aac cac aac tac     336
Ala Glu His Val Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr
            100             105             110

gcc aac gta tct ctc atc att gag atc gcc gag cgc ttc aac gtc gac     384
Ala Asn Val Ser Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp
            115             120             125

gcc gtc tgg gcc ggc tgg ggc cac gcc tct gag aat ccg ctt ctg ccc     432
Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro
        130             135             140
```

```
gac acg ctc gct cag act gag cgt aag atc gtc ttt atc ggc ccc ccg      480
Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro
145             150             155             160

ggc aag ccc atg cgt gca ttg ggc gac aag atc ggc tcc act atc atc      528
Gly Lys Pro Met Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile
            165             170             175

gcg cag agc gct aag gtg cct aca atc gcc tgg aac ggc gac ggc atg      576
Ala Gln Ser Ala Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met
            180             185             190

gaa gtc gac tac aag gaa cac gac gga atc ccc gac gag atc tac aac      624
Glu Val Asp Tyr Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn
            195             200             205

gcc gct atg ttg cgt gac ggc cag cac tgt ctg gac gaa tgc aaa cgt      672
Ala Ala Met Leu Arg Asp Gly Gln His Cys Leu Asp Glu Cys Lys Arg
            210             215             220

atc ggc ttc ccc gtc atg att aaa gcc agc gaa ggc gga ggt ggc aag      720
Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys
225             230             235             240

ggt atc cgt atg gtt cac gaa gag tcc cag gtg ctc agt gcc tgg gaa      768
Gly Ile Arg Met Val His Glu Glu Ser Gln Val Leu Ser Ala Trp Glu
            245             250             255

gct gtg cgt ggt gag atc cct ggg tct cct atc ttc gtc atg aag ctg      816
Ala Val Arg Gly Glu Ile Pro Gly Ser Pro Ile Phe Val Met Lys Leu
            260             265             270

gca ccc aag tcg cgt cac ttg gaa gtg cag cta ttg gcg gat acg tac      864
Ala Pro Lys Ser Arg His Leu Glu Val Gln Leu Leu Ala Asp Thr Tyr
            275             280             285

ggc aat gcc atc gct ctc agt ggc cgt gat tgc tcc gtg cag cgt cgt      912
Gly Asn Ala Ile Ala Leu Ser Gly Arg Asp Cys Ser Val Gln Arg Arg
            290             295             300

cac caa aag atc gtc gag gaa ggt ccc gtt ctt gcg ccc acc caa gaa      960
His Gln Lys Ile Val Glu Glu Gly Pro Val Leu Ala Pro Thr Gln Glu
305             310             315             320

gtg tgg gag aag atg atg cgc gcc gcc act cgc ctc gct cag gag gtc     1008
Val Trp Glu Lys Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val
            325             330             335

gag tac gtc aac gcc ggt acc gtc gag tac ctg ttc agt gag ctg ccg     1056
Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro
            340             345             350

gaa gac aac ggc aac tcg ttc ttc ttc ctg gaa ctc aac ccg cgt ttg     1104
Glu Asp Asn Gly Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu
            355             360             365

cag gtg gaa cac ccc gtc aca gag atg atc act cat gtg aat ctc cca     1152
Gln Val Glu His Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro
            370             375             380

gct gct caa ctg caa gtg gct atg ggt att ccg ctg cac tgc atc ccg     1200
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7

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Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro
385             390             395                 400

gat gtg cgt cgt ctg tac aac aag gat gcg ttt gag acg aca gtt att    1248
Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile
                405             410             415

gac ttc gac gcg gag aag cag aag cca ccg cat gga cac gtt atc gcc    1296
Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala
            420             425             430

gcg cgt att acc gcc gag gat ccg aac gcc ggt ttc cag cct acc agt    1344
Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser
            435             440             445

gga gcc atc cag gag ctt aac ttc cgt agt acg ccc gat gta tgg ggt    1392
Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly
    450             455             460

tac ttc tcg gtg gac tcg tcc gga cag gtg cac gag ttc gct gac tca    1440
Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser
465             470             475                 480

cag att ggt cac ctg ttc tcg tgg agt ccg act cgt gaa aag gcc cgt    1488
Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg
            485             490             495

aag aac atg gtt cta gcg ctc aag gag ttg tcg att cgt ggt gat att    1536
Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile
            500             505             510

cac acg acg gtc gag tac atc gtt aac atg atg gag tct gat gat ttc    1584
His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe
            515             520             525

aag tac aac cgc atc tcc acg tcg tgg ctg gat gag cgt atc tcg cac    1632
Lys Tyr Asn Arg Ile Ser Thr Ser Trp Leu Asp Glu Arg Ile Ser His
    530             535             540

cac aat gaa gtg cgt cta cag ggt cgg ccg gac                        1665
His Asn Glu Val Arg Leu Gln Gly Arg Pro Asp
545             550             555


<210>  4
<211>  555
<212>  PRT
<213>  Phytophthora infestans

<400>  4

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1               5               10              15


Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu
            20              25              30


Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile
        35              40              45
```

```
Ala Asn Asn Gly Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser
    50              55              60

Trp Ser Tyr Glu Met Phe Ala Asp Glu His Val Val Thr Phe Val Val
65              70              75              80

Met Ala Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met
                85              90              95

Ala Glu His Val Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr
            100             105             110

Ala Asn Val Ser Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp
        115             120             125

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro
        130             135             140

Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro
145             150             155             160

Gly Lys Pro Met Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile
            165             170             175

Ala Gln Ser Ala Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met
        180             185             190

Glu Val Asp Tyr Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn
        195             200             205

Ala Ala Met Leu Arg Asp Gly Gln His Cys Leu Asp Glu Cys Lys Arg
210             215             220

Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys
225             230             235             240

Gly Ile Arg Met Val His Glu Glu Ser Gln Val Leu Ser Ala Trp Glu
            245             250             255

Ala Val Arg Gly Glu Ile Pro Gly Ser Pro Ile Phe Val Met Lys Leu
            260             265             270

Ala Pro Lys Ser Arg His Leu Glu Val Gln Leu Leu Ala Asp Thr Tyr
        275             280             285
```

9

```
Gly Asn Ala Ile Ala Leu Ser Gly Arg Asp Cys Ser Val Gln Arg Arg
    290             295             300

His Gln Lys Ile Val Glu Glu Gly Pro Val Leu Ala Pro Thr Gln Glu
305             310             315             320

Val Trp Glu Lys Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val
                325             330             335

Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro
                340             345             350

Glu Asp Asn Gly Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu
        355             360             365

Gln Val Glu His Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro
    370             375             380

Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro
385             390             395             400

Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile
            405             410             415

Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala
            420             425             430

Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser
        435             440             445

Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly
    450             455             460

Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser
465             470             475             480

Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg
            485             490             495

Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile
            500             505             510

His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe
        515             520             525
```

```
Lys Tyr Asn Arg Ile Ser Thr Ser Trp Leu Asp Glu Arg Ile Ser His
    530                 535                 540

His Asn Glu Val Arg Leu Gln Gly Arg Pro Asp
545                 550                 555
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act gag aca aat gga acc gct gcg gct gct aac agc tcc cgt cag cgc        48
Thr Glu Thr Asn Gly Thr Ala Ala Ala Ala Asn Ser Ser Arg Gln Arg
1               5                   10                  15

aac ggc gcc aac ggc gtc acc gtg cct gtg gcc aac ggc aag gct act        96
Asn Gly Ala Asn Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr
                20                  25                  30

tac gct cag agg cac aag att gcc gac cac ttt att ggc ggc aac agg       144
Tyr Ala Gln Arg His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg
        35                  40                  45

cta gag aat gcc cct ccg tcc aag gtc aag gag tgg gtt gcc gca cac       192
Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His
    50                  55                  60

gac ggc cac aca gtc atc acc aac gtc ctg att gcc aac aac ggt atc       240
Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile
65                  70                  75                  80

gct gcc gtc aag gag att cga tcc gtg cga aaa tgg gca tac gag acg       288
Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr
                85                  90                  95

ttc gga gac gaa agg gcc att cag ttc act gtg atg gcc act ccc gag       336
Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu
                100                 105                 110

gat ttg caa gca aac gca gac tac att cgc atg gca gac cac tac gtc       384
Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val
        115                 120                 125

gag gtc cct ggt ggt aca aac aac aac aac tat gcg aac gtc gag ttg       432
Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu
    130                 135                 140

atc gtc gat gtt gcg gag cgc atg aac gtg cac gcc gtt tgg gcc ggt       480
Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly
145                 150                 155                 160

tgg gga cac gca tcg gag aac cca aag ctc cct gag tct ctc gct gcc       528
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```
Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala
            165                 170             175

tcg cct aag aaa att att ttc atc ggc cct ccc ggc tcc gcg atg cgc    576
Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg
            180                 185             190

tcg ctc ggt gac aag atc tct tct acc att gtc gct caa cat gcc cag    624
Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln
            195                 200             205

gtc cca tgt atc ccc tgg tcg gga act ggt gtt gat gcg gtc caa atc    672
Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile
    210                 215             220

gac aag aag gga att gtc acc gtc gac gac gac act tat gcc aaa gga    720
Asp Lys Lys Gly Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly
225             230             235                 240

tgc gtc act tca tgg cag gag ggt ctt gag aag gcc aga caa att ggt    768
Cys Val Thr Ser Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly
            245                 250             255

ttc ccg gtc atg atc aag gct tct gag ggt ggt ggt ggc aag ggt atc    816
Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
            260                 265             270

cgt aag gct gtc tcc gag gag ggc ttc gag gag ctc tac aag gcc gct    864
Arg Lys Ala Val Ser Glu Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala
            275                 280             285

gcc agt gaa atc ccc ggt tcg ccc atc ttc atc atg aag ctt gca ggc    912
Ala Ser Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly
            290                 295             300

aac gcc agg cat ttg gaa gtg cag ctt ctc gct gat cag tac ggc aac    960
Asn Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn
305             310             315                 320

aac atc tcc ctc ttt ggt cgt gat tgt tcc gtc cag cga agg cac caa   1008
Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
            325                 330             335

aag att atc gag gaa gct ccc gtg acc atc gcc aag ccc gac acg ttc   1056
Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Pro Asp Thr Phe
            340                 345             350

aag gcc atg gag gag gcc gct gtt cgt ctt ggt cgt ctt gtc ggt tac   1104
Lys Ala Met Glu Glu Ala Ala Val Arg Leu Gly Arg Leu Val Gly Tyr
            355                 360             365

gtc tct gct ggt acc gtc gag tac ctg tac tcg cac gcc gac gac aag   1152
Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys
    370                 375             380

ttc tac ttc ctg gag ctc aac cct cgt ctt cag gtc gag cat cct acc   1200
Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
385                 390             395                 400

act gag ggt gtc agt ggt gtc aac ctc ccc gct tcg cag ctt cag att   1248
Thr Glu Gly Val Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile
```

12

gcc atg ggt atc cct ctc cac agg ata tct gac att agg ctc ctt tac   1296
Ala Met Gly Ile Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr
            420   425   430

ggt gtg gac ccc aag ctc tcg act gag atc gac ttt gac ttc aag aac   1344
Gly Val Asp Pro Lys Leu Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn
            435   440   445

ccc gac agc gag aag acg cag agg agg cca tcg ccc aaa ggc cac ctt   1392
Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu
            450   455   460

act gcc tgc cgt att acc tca gag gac cct gga gag ggc ttc aag ccg   1440
Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro
465   470   475   480

tcc aac ggt gtc atg cac gag ctg aac ttc cgc agt agt tca aac gtg   1488
Ser Asn Gly Val Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val
            485   490   495

tgg ggt tac ttc tca gtc ggt acg cag ggt gga att cac agt ttc tcc   1536
Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser
            500   505   510

gac agt cag ttc ggt cac att ttc gcc tat ggc gag aac cga tcc gcg   1584
Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala
            515   520   525

tca agg aag cac atg gtt atc gcc ttg aag gaa ctt agc att cgt ggt   1632
Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly
            530   535   540

gat ttc cgc acc acg gtc gag tac cta atc aag ctt ctg gag acg gag   1680
Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu
545   550   555   560

gct ttc gag gag aac acc att acc act ggc tgg ctg gac gag ctt att   1728
Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile
            565   570   575

tcg aag aag ctc act gcg gag agg ccc gac aag atg ctt gct gtt   1773
Ser Lys Lys Leu Thr Ala Glu Arg Pro Asp Lys Met Leu Ala Val
            580   585   590

<210> 6
<211> 591
<212> PRT
<213> Magnaporthe grisea

<400> 6

Thr Glu Thr Asn Gly Thr Ala Ala Ala Ala Asn Ser Ser Arg Gln Arg
1   5   10   15

Asn Gly Ala Asn Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr
            20   25   30

```
Tyr Ala Gln Arg His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg
        35                  40                  45

Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His
        50                  55                  60

Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile
65                  70                  75                  80

Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr
                85                  90                  95

Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu
                100                 105                 110

Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val
        115                 120                 125

Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu
        130                 135                 140

Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly
145                 150                 155                 160

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala
                165                 170                 175

Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg
                180                 185                 190

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln
        195                 200                 205

Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile
210                 215                 220

Asp Lys Lys Gly Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly
225                 230                 235                 240

Cys Val Thr Ser Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly
                245                 250                 255

Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
                260                 265                 270
```

14

Arg Lys Ala Val Ser Glu Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala
        275   280   285

Ala Ser Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly
        290   295   300

Asn Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn
305   310   315   320

Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
                325   330   335

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Pro Asp Thr Phe
                340   345   350

Lys Ala Met Glu Glu Ala Ala Val Arg Leu Gly Arg Leu Val Gly Tyr
        355   360   365

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys
    370   375   380

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
385   390   395   400

Thr Glu Gly Val Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile
                405   410   415

Ala Met Gly Ile Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr
                420   425   430

Gly Val Asp Pro Lys Leu Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn
        435   440   445

Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu
    450   455   460

Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro
465   470   475   480

Ser Asn Gly Val Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val
        485   490   495

Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser
        500   505   510

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala

```
Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly
    530                 535             540
```

```
Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu
545             550             555             560
```

```
Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile
            565             570             575
```

```
Ser Lys Lys Leu Thr Ala Glu Arg Pro Asp Lys Met Leu Ala Val
            580             585             590
```

<210> 7
<211> 1740
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (1)..(1740)
<223> ACCase BC domain (aa 2-581)

<220>
<221> misc_feature
<222> (226)..(228)
<223> Alteration of Ser-77 codon results in Ser to Tyr mutation that
      eliminates soraphen binding

<400> 7
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tct gaa gaa agc tta ttc gag tct tct cca cag aag atg gag tac gaa      48
Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1                 5                   10                  15

att aca aac tac tca gaa aga cat aca gaa ctt cca ggt cat ttc att      96
Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile
                20                  25                  30

ggc ctc aat aca gta gat aaa cta gag gag tcc ccg tta agg gac ttt     144
Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe
            35                  40                  45

gtt aag agt cac ggt ggt cac acg gtc ata tcc aag atc ctg ata gca     192
Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala
    50                  55                  60

aat aat ggt att gcc gcc gtg aaa gaa att aga tcc gtc aga aaa tgg     240
Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp
65                  70                  75                  80

gca tac gag acg ttc ggc gat gac aga acc gtc caa ttc gtc gcc atg     288
Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met
                85                  90                  95
```

```
gcc acc cca gaa gat ctg gag gcc aac gca gaa tat atc cgt atg gcc          336
Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala
            100             105             110

gat caa tac att gaa gtg cca ggt ggt act aat aat aac aac tac gct          384
Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala
            115             120             125

aac gta gac ttg atc gta gac atc gcc gaa aga gca gac gta gac gcc          432
Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala
130             135             140

gta tgg gct ggc tgg ggt cac gcc tcc gag aat cca cta ttg cct gaa          480
Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu
145             150             155             160

aaa ttg tcc cag tct aag agg aaa gtc atc ttt att ggg cct cca ggt          528
Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly
                165             170             175

aac gcc atg agg tct tta ggt gat aaa atc tcc tct acc att gtc gct          576
Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala
                180             185             190

caa agt gct aaa gtc cca tgt att cca tgg tct ggt acc ggt gtt gac          624
Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp
            195             200             205

acc gtt cac gtg gac gag aaa acc ggt ctg gtc tct gtc gac gat gac          672
Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp
            210             215             220

atc tat caa aag ggt tgt tgt acc tct cct gaa gat ggt tta caa aag          720
Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys
225             230             235             240

gcc aag cgt att ggt ttt cct gtc atg att aag gca tcc gaa ggt ggt          768
Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly
                245             250             255

ggt ggt aaa ggt atc aga caa gtt gaa cgt gaa gaa gat ttc atc gct          816
Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala
                260             265             270

tta tac cac cag gca gcc aac gaa att cca ggc tcc ccc att ttc atc          864
Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile
            275             280             285

atg aag ttg gcc ggt aga gcg cgt cac ttg gaa gtt caa ctg cta gca          912
Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala
            290             295             300

gat cag tac ggt aca aat att tcc ttg ttc ggt aga gac tgt tcc gtt          960
Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val
305             310             315             320

cag aga cgt cat caa aaa att atc gaa gaa gca cca gtt aca att gcc         1008
Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala
            325             330             335

aag gct gaa aca ttt cac gag atg gaa aag gct gcc gtc aga ctg ggg         1056
```

```
Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly
            340                 345                 350

aaa cta gtc ggt tat gtc tct gcc ggt acc gtg gag tat cta tat tct        1104
Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser
            355                 360                 365

cat gat gat gga aaa ttc tac ttt tta gaa ttg aac cca aga tta caa        1152
His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln
            370                 375                 380

gtc gag cat cca aca acg gaa atg gtc tcc ggt gtt aac tta cct gca        1200
Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala
385                 390                 395                 400

gct caa tta caa atc gct atg ggt atc cct atg cat aga ata agt gac        1248
Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp
                405                 410                 415

att aga act tta tat ggt atg aat cct cat tct gcc tca gaa atc gat        1296
Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp
                420                 425                 430

ttc gaa ttc aaa act caa gat gcc acc aag aaa caa aga aga cct att        1344
Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile
            435                 440                 445

cca aag ggt cat tgt acc gct tgt cgt atc aca tca gaa gat cca aac        1392
Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn
            450                 455                 460

gat gga ttc aag cca tcg ggt ggt act ttg cat gaa cta aac ttc cgt        1440
Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg
465                 470                 475                 480

tct tcc tct aat gtt tgg ggt tac ttc tcc gtg ggt aac aat ggt aat        1488
Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn
                485                 490                 495

att cac tcc ttt tcg gac tct cag ttc ggc cat att ttt gct ttt ggt        1536
Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly
                500                 505                 510

gaa aat aga caa gct tcc agg aaa cac atg gtt gtt gcc ctg aag gaa        1584
Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu
            515                 520                 525

ttg tcc att agg ggt gat ttc aga act act gtg gaa tac ttg atc aaa        1632
Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
            530                 535                 540

ctt ttg gaa act gaa gat ttc gag gat aac act att acc acc ggt tgg        1680
Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp
545                 550                 555                 560

ttg gac gat ttg att act cat aaa atg acc gct gaa aag cct gat cca        1728
Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro
                565                 570                 575

act ctt gcc gtc                                                        1740
Thr Leu Ala Val
```

18

580

<210>   8
<211>   580
<212>   PRT
<213>   Saccharomyces cerevisiae

<400>   8

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1   5   10   15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile
            20   25   30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe
            35   40   45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala
        50   55   60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp
65   70   75   80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met
                85   90   95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala
            100   105   110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala
            115   120   125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala
        130   135   140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu
145   150   155   160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly
                165   170   175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala
            180   185   190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp
        195   200   205

19

```
Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp
    210                 215                 220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys
225                 230                 235                 240

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly
                245                 250                 255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala
                260                 265                 270

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile
                275                 280                 285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala
    290                 295                 300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val
305                 310                 315                 320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala
                325                 330                 335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly
                340                 345                 350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser
                355                 360                 365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln
                370                 375                 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala
385                 390                 395                 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp
                405                 410                 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp
                420                 425                 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile
                435                 440                 445
```

20

```
Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn
    450                 455                 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg
465                 470                 475                 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn
                485                 490                 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly
                500                 505                 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu
            515                 520                 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
    530                 535                 540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp
545                 550                 555                 560

Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro
                565                 570                 575

Thr Leu Ala Val
            580


<210>   9
<211>   1896
<212>   DNA
<213>   Homo sapiens


<220>
<221>   CDS
<222>   (1)..(1896)
<223>   Human ACCase1 (alpha) BC domain (aa 1-632)

<400>   9
atg gat gaa cca tct ccc ttg gcc caa cct ctg gag ctg aac cag cac     48
Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His
1               5                   10                  15

tct cga ttc ata ata ggt tct gtg tct gaa gat aac tca gag gat gag     96
Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
                20                  25                  30

atc agc aac ctg gtg aag ttg gac cta ctg gag gag aag gag ggc tcc    144
Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
            35                  40                  45

ttg tca cct gct tct gtt ggc tca gat aca ctc tct gat ttg ggg atc    192
```

```
Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
    50              55                  60

tct agc cta cag gat ggc ttg gcc ttg cac ata agg tcc agc atg tct        240
Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser
65              70                  75                  80

ggc ttg cac cta gta aag cag ggc cga gac aga aag aaa ata gat tct        288
Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser
                85                  90                  95

caa cga gat ttc act gtg gct tct cca gca gaa ttt gtt act cgc ttt        336
Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe
            100                 105                 110

ggg gga aat aaa gtg att gag aag gtt ctt att gct aac aat ggc att        384
Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile
            115                 120                 125

gca gca gtg aaa tgc atg cgg tct atc cgt agg tgg tct tat gaa atg        432
Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met
    130                 135                 140

ttt cga aat gaa cgt gca att aga ttc gtt gtc atg gtc aca cct gaa        480
Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu
145                 150                 155                 160

gac ctt aaa gcc aat gca gaa tac att aag atg gca gat cac tat gtg        528
Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val
                165                 170                 175

cca gtg cct gga gga cca aac aac aac aac tat gca aat gtg gaa tta        576
Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu
            180                 185                 190

att ctt gat att gct aaa agg atc cca gtg cag gca gtg tgg gct ggc        624
Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly
            195                 200                 205

tgg ggt cat gct tct gag aat ccc aaa cta ccg gaa ctt ctc ttg aaa        672
Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys
    210                 215                 220

aat ggc att gcc ttc atg ggt cct cca agc cag gcc atg tgg gct tta        720
Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu
225                 230                 235                 240

ggg gat aag att gca tct tcc ata gtg gct caa act gca ggt atc cca        768
Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro
            245                 250                 255

act ctt ccc tgg agc ggc agt ggt ctt cgt gtg gac tgg cag gaa aat        816
Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn
            260                 265                 270

gat ttt tca aaa cgt atc tta aat gtt ccc cag gag cta tat gaa aaa        864
Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys
            275                 280                 285

ggt tat gtg aaa gat gtg gat gat ggg cta aag gca gct gag gaa gtt        912
Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val
```

```
        290                      295                      300

gga tat cca gta atg atc aag gcc tca gag gga gga gga ggg aag gga        960
Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly
305                 310                 315                 320

att aga aaa gtc aac aat gca gat gac ttc cct aat ctc ttc aga cag       1008
Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln
                325                 330                 335

gtt caa gct gaa gtt cct gga tct ccc ata ttt gtg atg aga cta gcc      1056
Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala
                340                 345                 350

aaa caa tct cgt cat ctg gag gtg cag atc tta gcg gac caa tat ggc      1104
Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly
                355                 360                 365

aat gct atc tct ttg ttt ggt cgt gat tgc tct gta caa cgc agg cat      1152
Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His
        370                 375                 380

cag aag att att gaa gaa gca cct gct act att gct act cca gca gta      1200
Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val
385                 390                 395                 400

ttt gaa cac atg gaa cag tgt gcg gtg aaa ctt gcc aaa atg gtg ggt      1248
Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly
                405                 410                 415

tat gtg agt gct ggg act gtg gaa tac ctg tac agc cag gat ggc agc      1296
Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser
                420                 425                 430

ttc tac ttt ctg gaa ttg aat cct cgg ctg cag gta gag cac cct tgt      1344
Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys
        435                 440                 445

aca gag atg gtg gct gat gtc aat ctc cct gca gca cag ctc cag att      1392
Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile
450                 455                 460

gcc atg ggg att cct cta tat aga atc aag gat atc cgt atg atg tat      1440
Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr
465                 470                 475                 480

ggg gta tct ccc tgg ggt gat tct ccc att gat ttt gaa gat tct gca      1488
Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala
                485                 490                 495

cac gtt cct tgt cca agg ggc cat gtt att gct gct cgg atc act agt      1536
His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser
                500                 505                 510

gaa aat cca gat gag ggt ttt aag ccc agc tca gga aca gtt cag gag      1584
Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu
                515                 520                 525

cta aat ttc cgc agc aat aag aat gtt tgg gga tat ttc agt gtt gct      1632
Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala
        530                 535                 540
```

23

```
gct gca ggg gga ctt cat gaa ttt gct gat tct cag ttt ggt cac tgc      1680
Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys
545                 550                 555                 560

ttt tct tgg gga gaa aac aga gaa gag gca att tca aac atg gtg gtg      1728
Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val
                565                 570                 575

gct ttg aag gag ctg tct att cgg ggt gac ttt cga act aca gtt gaa      1776
Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu
                580                 585                 590

tac ctg atc aaa ttg tta gag act gaa agc ttt cag atg aac aga att      1824
Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile
            595                 600                 605

gat act ggc tgg ctg gac aga ctg ata gca gaa aaa gta cag gct gag      1872
Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu
        610                 615                 620

cga cct gac acc atg ttg ggg gtt                                      1896
Arg Pro Asp Thr Met Leu Gly Val
625                 630


<210>   10
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<212>   PRT
<213>   Homo sapiens

<400>   10

Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His
1               5                   10                  15


Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
                20                  25                  30


Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
            35                  40                  45


Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
        50                  55                  60


Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser
65                  70                  75                  80


Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser
                85                  90                  95


Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe
                100                 105                 110
```

24

Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile
        115   120   125

Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met
    130   135   140

Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu
145   150   155   160

Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val
                165   170   175

Pro Val Pro Gly Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu
            180   185   190

Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly
        195   200   205

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys
    210   215   220

Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu
225   230   235   240

Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro
            245   250   255

Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn
            260   265   270

Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys
        275   280   285

Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val
    290   295   300

Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly
305   310   315   320

Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln
            325   330   335

Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala
            340   345   350

Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly

25

Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His
    370   375   380

Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val
385   390   395   400

Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly
                405   410   415

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser
            420   425   430

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys
        435   440   445

Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile
    450   455   460

Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr
465   470   475   480

Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala
            485   490   495

His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser
            500   505   510

Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu
        515   520   525

Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala
    530   535   540

Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys
545   550   555   560

Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val
            565   570   575

Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu
        580   585   590

Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile
        595   600   605

```
Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu
    610                 615                 620

Arg Pro Asp Thr Met Leu Gly Val
625                 630


<210>  11
<211>  2322
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(2322)
<223>  Human ACCase2 (beta) BC domain (aa 1-774)

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atg gtc ttg ctt ctt tgt cta tct tgt ctg att ttc tcc tgt ctg acc      48
Met Val Leu Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr
1               5                   10                  15

ttt tcc tgg tta aaa atc tgg ggg aaa atg acg gac tcc aag ccg atc      96
Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile
            20                  25                  30

acc aag agt aaa tca gaa gca aac ctc atc ccg agc cag gag ccc ttt     144
Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe
        35                  40                  45

cca gcc tct gat aac tca ggg gag aca ccg cag aga aat ggg gag ggc     192
Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly
    50                  55                  60

cac act ctg ccc aag aca ccc agc cag gcc gag cca gcc tcc cac aaa     240
His Thr Leu Pro Lys Thr Pro Ser Gln Ala Glu Pro Ala Ser His Lys
65                  70                  75                  80

ggc ccc aaa gat gcc ggt cgg cgg aga aac tcc cta cca ccc tcc cac     288
Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His
            85                  90                  95

cag aag ccc cca aga aac ccc ctt tct tcc agt gac gca gca ccc tcc     336
Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser
            100                 105                 110

cca gag ctt caa gcc aac ggg act ggg aca caa ggt ctg gag gcc aca     384
Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr
            115                 120                 125

gat acc aat ggc ctg tcc tcc tca gcc agg ccc cag ggc cag caa gct     432
Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala
    130                 135                 140

ggc tcc ccc tcc aaa gaa gac aag aag cag gca aac atc aag agg cag     480
Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln
145                 150                 155                 160
```

27

```
ctg atg acc aac ttc atc ctg ggc tct ttt gat gac tac tcc tct gac    528
Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp
            165             170             175

gag gac tct gtt gct ggc tca tct cgt gag tct acc cgg aag ggc agc    576
Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser
            180             185             190

cgg gcc agc ttg ggg gcc ctg tcc ctg gag gct tat ctg acc aca ggt    624
Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly
            195             200             205

gaa gct gag acc cgc gtc ccc act atg agg ccg agc atg tcg gga ctc    672
Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu
            210             215             220

cac ctg gtg aag agg gga cgg gaa cac aag aag ctg gac ctg cac aga    720
His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg
225             230             235             240

gac ttt acc gtg gct tct ccc gct gag ttt gtc aca cgc ttt ggg ggg    768
Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly
            245             250             255

gat cgg gtc atc gag aag gtg ctt att gcc aac aac ggg att gcc gcc    816
Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala
            260             265             270

gtg aag tgc atg cgc tcc atc cgc agg tgg gcc tat gag atg ttc cgc    864
Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg
            275             280             285

aac gag cgg gcc atc cgg ttt gtt gtg atg gtg acc ccc gag gac ctt    912
Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu
            290             295             300

aag gcc aac gca gag tac atc aag atg gcg gat cat tac gtc ccc gtc    960
Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val
305             310             315             320

cca gga ggg ccc aat aac aac aac tat gcc aac gtg gag ctg att gtg    1008
Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val
            325             330             335

gac att gcc aag aga att cct ttg cag gcg gtg tgg gct ggc tgg ggc    1056
Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly
            340             345             350

cat gct tca gaa aac cct aaa ctt ccg gag ctg ctg tgc aag aat gga    1104
His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly
            355             360             365

gtt gct ttc tta ggc cct ccc agt gag gcc atg tgg gcc tta gga gat    1152
Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp
            370             375             380

aag atc gcc tcc acc gtt gtc gcc cag acg cta cag gtc cca acc ctg    1200
Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu
385             390             395             400
```

28

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ccc agg agt gga agc ggc ctg aca gtg gag tgg aca gaa gat gat ctg        1248
Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu
            405             410             415

cag cag gga aaa aga atc agt gtc cca gaa gat gtt tat gac aag ggt        1296
Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly
            420             425             430

tgc gtg aaa gac gta gat gag ggc ttg gag gca gca gaa aga att ggt        1344
Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly
            435             440             445

ttt cca ttg atg atc aaa gct tct gaa ggt ggc gga ggg aag gga atc        1392
Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
    450             455             460

cgg aag gct gag agt gcg gag gac ttc ccg atc ctt ttc aga caa gta        1440
Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val
465             470             475             480

cag agt gag atc cca ggc tcg ccc atc ttt ctc atg aag ctg gcc cag        1488
Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln
            485             490             495

cac gcc cgt cac ctg gaa gtt cag atc ctc gct gac cag tat ggg aat        1536
His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn
            500             505             510

gct gtg tct ctg ttt ggt cgc gac tgc tcc atc cag cgg cgg cat cag        1584
Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln
            515             520             525

aag atc gtt gag gaa gca ccg gcc acc atc gcc ccg ctg gcc ata ttc        1632
Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe
            530             535             540

gag ttc atg gag cag tgt gcc atc cgc ctg gcc aag acc gtg ggc tat        1680
Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr
545             550             555             560

gtg agt gca ggg aca gtg gaa tac ctc tat agt cag gat ggc agc ttc        1728
Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe
            565             570             575

cac ttc ttg gag ctg aat cct cgc ttg cag gtg gaa cat ccc tgc aca        1776
His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr
            580             585             590

gaa atg att gct gat gtt aat ctg ccg gcc gcc cag cta cag atc gcc        1824
Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala
            595             600             605

atg ggc gtg cca ctg cac cgg ctg aag gat atc cgg ctt ctg tat gga        1872
Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly
            610             615             620

gag tca cca tgg gga gtg act ccc att tct ttt gaa acc ccc tca aac        1920
Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn
625             630             635             640

cct ccc ctc gcc cga ggc cac gtc att gcc gcc aga atc acc agc gaa        1968
```

29

```
Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu
            645             650             655

aac cca gac gag ggt ttt aag ccg agc tcc ggg act gtc cag gaa ctg    2016
Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu
            660             665             670

aat ttc cgg agc agc aag aac gtg tgg ggt tac ttc agc gtg gcc gct    2064
Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala
            675             680             685

act gga ggc ctg cac gag ttt gcg gat tcc caa ttt ggg cac tgc ttc    2112
Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe
            690             695             700

tcc tgg gga gag aac cgg aaa gag gcc att tcg aac atg gtg gtg gct    2160
Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala
705             710             715             720

ttg aag gaa ctg tcc atc cga ggt gac ttt agg act acc gtg gaa tac    2208
Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr
            725             730             735

ctc att aac ctc ctg gag acc gag agc ttc cag aac aac gac atc gac    2256
Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp
            740             745             750

acc ggg tgg ttg gac tac ctc att gct gag aaa gtg cag gag aaa ccg    2304
Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Glu Lys Pro
            755             760             765

gat atc atg ctt ggg gtg                                            2322
Asp Ile Met Leu Gly Val
            770


<210>  12
<211>  774
<212>  PRT
<213>  Homo sapiens

<400>  12

Met Val Leu Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr
1               5               10              15


Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile
            20              25              30


Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe
            35              40              45


Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly
            50              55              60


His Thr Leu Pro Lys Thr Pro Ser Gln Ala Glu Pro Ala Ser His Lys
65              70              75              80
```

Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His
            85   90   95

Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser
            100   105   110

Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr
            115   120   125

Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala
            130   135   140

Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln
145   150   155   160

Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp
            165   170   175

Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser
            180   185   190

Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly
            195   200   205

Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu
210   215   220

His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg
225   230   235   240

Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly
            245   250   255

Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala
            260   265   270

Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg
            275   280   285

Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu
            290   295   300

Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val
305   310   315   320

31

Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val
              325   330   335

Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly
              340   345   350

His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly
              355   360   365

Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp
    370   375   380

Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu
385   390   395   400

Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu
              405   410   415

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly
              420   425   430

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly
              435   440   445

Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
    450   455   460

Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val
465   470   475   480

Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln
              485   490   495

His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn
              500   505   510

Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln
              515   520   525

Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe
    530   535   540

Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr
545   550   555   560

32

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe
                565   570   575

His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr
                580   585   590

Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala
                595   600   605

Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly
        610   615   620

Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn
625   630   635   640

Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu
                645   650   655

Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu
                660   665   670

Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala
                675   680   685

Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe
        690   695   700

Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala
705   710   715   720

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr
                725   730   735

Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp
                740   745   750

Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Glu Lys Pro
        755   760   765

Asp Ile Met Leu Gly Val
        770

<210>   13
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<212>   DNA
<213>   Homo sapiens

33

<220>
<221> CDS
<222> (1)..(1596)
<223> N-terminal deleted Human ACCase1 BC domain (AAs 102-632)

<400> 13

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atg gtg gct tct cca gca gaa ttt gtt act cgc ttt ggg gga aat aaa        48
Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys
1               5                   10                  15

gtg att gag aag gtt ctt att gct aac aat ggc att gca gca gtg aaa        96
Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
                20                  25                  30

tgc atg cgg tct atc cgt agg tgg tct tat gaa atg ttt cga aat gaa       144
Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu
            35                  40                  45

cgt gca att aga ttc gtt gtc atg gtc aca cct gaa gac ctt aaa gcc       192
Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala
        50                  55                  60

aat gca gaa tac att aag atg gca gat cac tat gtg cca gtg cct gga       240
Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly
65                  70                  75                  80

gga cca aac aac aac aac tat gca aat gtg gaa tta att ctt gat att       288
Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile
                85                  90                  95

gct aaa agg atc cca gtg cag gca gtg tgg gct ggc tgg ggt cat gct       336
Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala
                100                 105                 110

tct gag aat ccc aaa cta ccg gaa ctt ctc ttg aaa aat ggc att gcc       384
Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala
            115                 120                 125

ttc atg ggt cct cca agc cag gcc atg tgg gct tta ggg gat aag att       432
Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile
        130                 135                 140

gca tct tcc ata gtg gct caa act gca ggt atc cca act ctt ccc tgg       480
Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp
145                 150                 155                 160

agc ggc agt ggt ctt cgt gtg gac tgg cag gaa aat gat ttt tca aaa       528
Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys
                165                 170                 175

cgt atc tta aat gtt ccc cag gag cta tat gaa aaa ggt tat gtg aaa       576
Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys
                180                 185                 190

gat gtg gat gat ggg cta aag gca gct gag gaa gtt gga tat cca gta       624
Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val
                195                 200                 205

atg atc aag gcc tca gag gga gga gga ggg aag gga att aga aaa gtc       672
Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Val
```

34

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aac aat gca gat gac ttc cct aat ctc ttc aga cag gtt caa gct gaa      720
Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln Val Gln Ala Glu
225                 230                 235                 240

gtt cct gga tct ccc ata ttt gtg atg aga cta gcc aaa caa tct cgt      768
Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala Lys Gln Ser Arg
                    245                 250                 255

cat ctg gag gtg cag atc tta gcg gac caa tat ggc aat gct atc tct      816
His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser
                260                 265                 270

ttg ttt ggt cgt gat tgc tct gta caa cgc agg cat cag aag att att      864
Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile
                275                 280                 285

gaa gaa gca cct gct act att gct act cca gca gta ttt gaa cac atg      912
Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val Phe Glu His Met
                290                 295                 300

gaa cag tgt gcg gtg aaa ctt gcc aaa atg gtg ggt tat gtg agt gct      960
Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly Tyr Val Ser Ala
305                 310                 315                 320

ggg act gtg gaa tac ctg tac agc cag gat ggc agc ttc tac ttt ctg     1008
Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe Tyr Phe Leu
                    325                 330                 335

gaa ttg aat cct cgg ctg cag gta gag cac cct tgt aca gag atg gtg     1056
Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Val
                340                 345                 350

gct gat gtc aat ctc cct gca gca cag ctc cag att gcc atg ggg att     1104
Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile
                355                 360                 365

cct cta tat aga atc aag gat atc cgt atg atg tat ggg gta tct ccc     1152
Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr Gly Val Ser Pro
                370                 375                 380

tgg ggt gat tct ccc att gat ttt gaa gat tct gca cac gtt cct tgt     1200
Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala His Val Pro Cys
385                 390                 395                 400

cca agg ggc cat gtt att gct gct cgg atc act agt gaa aat cca gat     1248
Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp
                405                 410                 415

gag ggt ttt aag ccc agc tca gga aca gtt cag gag cta aat ttc cgc     1296
Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg
                420                 425                 430

agc aat aag aat gtt tgg gga tat ttc agt gtt gct gct gca ggg gga     1344
Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Ala Gly Gly
                435                 440                 445

ctt cat gaa ttt gct gat tct cag ttt ggt cac tgc ttt tct tgg gga     1392
Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly
                450                 455                 460
```

```
gaa aac aga gaa gag gca att tca aac atg gtg gtg gct ttg aag gag          1440
Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu
465                 470                 475                 480

ctg tct att cgg ggt gac ttt cga act aca gtt gaa tac ctg atc aaa          1488
Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
                485                 490                 495

ttg tta gag act gaa agc ttt cag atg aac aga att gat act ggc tgg          1536
Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp
                500                 505                 510

ctg gac aga ctg ata gca gaa aaa gta cag gct gag cga cct gac acc          1584
Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu Arg Pro Asp Thr
            515                 520                 525

atg ttg ggg gtt                                                          1596
Met Leu Gly Val
        530


<210>  14
<211>  532
<212>  PRT
<213>  Homo sapiens

<400>  14

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys
1               5                   10                  15


Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
                20                  25                  30


Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu
            35                  40                  45


Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala
        50                  55                  60


Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly
65                  70                  75                  80


Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile
                85                  90                  95


Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala
            100                 105                 110


Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala
            115                 120                 125
```

36

Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile
    130   135   140

Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp
145   150   155   160

Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys
                165   170   175

Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys
                180   185   190

Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val
                195   200   205

Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Val
    210   215   220

Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln Val Gln Ala Glu
225   230   235   240

Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala Lys Gln Ser Arg
                245   250   255

His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser
                260   265   270

Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile
                275   280   285

Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val Phe Glu His Met
    290   295   300

Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly Tyr Val Ser Ala
305   310   315   320

Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe Tyr Phe Leu
                325   330   335

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Val
                340   345   350

Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile
                355   360   365

Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr Gly Val Ser Pro

37

```
Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala His Val Pro Cys
385             390             395             400


Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp
            405             410             415


Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg
            420             425             430


Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Ala Gly Gly
            435             440             445


Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly
    450             455             460


Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu
465             470             475             480


Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
            485             490             495


Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp
            500             505             510


Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu Arg Pro Asp Thr
            515             520             525


Met Leu Gly Val
        530
```

```
<210>   15
<211>   1596
<212>   DNA
<213>   Homo sapiens


<220>
<221>   CDS
<222>   (1)..(1596)
<223>   N-terminal deleted Human ACCase2 BC domain (AAs 244-774)


<400>   15
atg gtg gct tct ccc gct gag ttt gtc aca cgc ttt ggg ggg gat cgg      48
Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg
1               5               10              15


gtc atc gag aag gtg ctt att gcc aac aac ggg att gcc gcc gtg aag      96
Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
```

```
tgc atg cgc tcc atc cgc agg tgg gcc tat gag atg ttc cgc aac gag      144
Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu
        35                  40                  45

cgg gcc atc cgg ttt gtt gtg atg gtg acc ccc gag gac ctt aag gcc      192
Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala
    50                  55                  60

aac gca gag tac atc aag atg gcg gat cat tac gtc ccc gtc cca gga      240
Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly
65                  70                  75                  80

ggg ccc aat aac aac aac tat gcc aac gtg gag ctg att gtg gac att      288
Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile
                85                  90                  95

gcc aag aga att cct ttg cag gcg gtg tgg gct ggc tgg ggc cat gct      336
Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala
                100                 105                 110

tca gaa aac cct aaa ctt ccg gag ctg ctg tgc aag aat gga gtt gct      384
Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala
            115                 120                 125

ttc tta ggc cct ccc agt gag gcc atg tgg gcc tta gga gat aag atc      432
Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile
        130                 135                 140

gcc tcc acc gtt gtc gcc cag acg cta cag gtc cca acc ctg ccc agg      480
Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg
145                 150                 155                 160

agt gga agc ggc ctg aca gtg gag tgg aca gaa gat gat ctg cag cag      528
Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln
                165                 170                 175

gga aaa aga atc agt gtc cca gaa gat gtt tat gac aag ggt tgc gtg      576
Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val
            180                 185                 190

aaa gac gta gat gag ggc ttg gag gca gca gaa aga att ggt ttt cca      624
Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly Phe Pro
        195                 200                 205

ttg atg atc aaa gct tct gaa ggt ggc gga ggg aag gga atc cgg aag      672
Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys
        210                 215                 220

gct gag agt gcg gag gac ttc ccg atc ctt ttc aga caa gta cag agt      720
Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser
225                 230                 235                 240

gag atc cca ggc tcg ccc atc ttt ctc atg aag ctg gcc cag cac gcc      768
Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala
                245                 250                 255

cgt cac ctg gaa gtt cag atc ctc gct gac cag tat ggg aat gct gtg      816
Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val
                260                 265                 270
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tct ctg ttt ggt cgc gac tgc tcc atc cag cgg cgg cat cag aag atc     864
Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile
        275             280             285

gtt gag gaa gca ccg gcc acc atc gcc ccg ctg gcc ata ttc gag ttc     912
Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe
        290             295             300

atg gag cag tgt gcc atc cgc ctg gcc aag acc gtg ggc tat gtg agt     960
Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser
305             310             315             320

gca ggg aca gtg gaa tac ctc tat agt cag gat ggc agc ttc cac ttc    1008
Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe
                325             330             335

ttg gag ctg aat cct cgc ttg cag gtg gaa cat ccc tgc aca gaa atg    1056
Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met
            340             345             350

att gct gat gtt aat ctg ccg gcc gcc cag cta cag atc gcc atg ggc    1104
Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly
        355             360             365

gtg cca ctg cac cgg ctg aag gat atc cgg ctt ctg tat gga gag tca    1152
Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser
        370             375             380

cca tgg gga gtg act ccc att tct ttt gaa acc ccc tca aac cct ccc    1200
Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro
385             390             395             400

ctc gcc cga ggc cac gtc att gcc gcc aga atc acc agc gaa aac cca    1248
Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro
            405             410             415

gac gag ggt ttt aag ccg agc tcc ggg act gtc cag gaa ctg aat ttc    1296
Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe
            420             425             430

cgg agc agc aag aac gtg tgg ggt tac ttc agc gtg gcc gct act gga    1344
Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly
            435             440             445

ggc ctg cac gag ttt gcg gat tcc caa ttt ggg cac tgc ttc tcc tgg    1392
Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp
        450             455             460

gga gag aac cgg aaa gag gcc att tcg aac atg gtg gtg gct ttg aag    1440
Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys
465             470             475             480

gaa ctg tcc atc cga ggt gac ttt agg act acc gtg gaa tac ctc att    1488
Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile
                485             490             495

aac ctc ctg gag acc gag agc ttc cag aac aac gac atc gac acc ggg    1536
Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly
                500             505             510
```

```
tgg ttg gac tac ctc att gct gag aaa gtg cag gag aaa ccg gat atc          1584
Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Glu Lys Pro Asp Ile
        515             520             525

atg ctt ggg gtg                                                          1596
Met Leu Gly Val
        530


<210>   16
<211>   532
<212>   PRT
<213>   Homo sapiens

<400>   16

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg
1               5               10              15


Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
            20              25              30


Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu
        35              40              45


Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala
    50              55              60


Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly
65              70              75              80


Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile
            85              90              95


Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala
            100             105             110


Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala
        115             120             125


Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile
    130             135             140


Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg
145             150             155             160


Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln
            165             170             175


Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val
```

41

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                     180                       185                       190

Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly Phe Pro
        195                 200                 205

Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys
    210                 215                 220

Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser
225                 230                 235                 240

Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala
            245                 250                 255

Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val
            260                 265                 270

Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile
        275                 280                 285

Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe
    290                 295                 300

Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser
305                 310                 315                 320

Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe
            325                 330                 335

Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met
            340                 345                 350

Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly
        355                 360                 365

Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser
    370                 375                 380

Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro
385                 390                 395                 400

Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro
            405                 410                 415

Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe
            420                 425                 430
```

Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly
        435   440   445

Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp
    450   455   460

Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys
465   470   475   480

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile
            485   490   495

Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly
            500   505   510

Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Glu Lys Pro Asp Ile
        515   520   525

Met Leu Gly Val
    530

<210> 17
<211> 554
<212> PRT
<213> Ustilago maydis

<220>
<221> MISC_FEATURE
<222> (1)..(554)
<223> N-terminal deleted Ustilago ACCase BC domain (AAs 7-560)

<400> 17

Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro
1   5   10   15

Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val
            20   25   30

Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu
        35   40   45

Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg
    50   55   60

Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn
65   70   75   80

43

Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly
            85   90   95

Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala
            100   105   110

Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser
        115   120   125

Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile
        130   135   140

Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys
145   150   155   160

Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met Pro
                165   170   175

Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe
            180   185   190

Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr Ala
        195   200   205

Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met Ile
210   215   220

Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr Asn
225   230   235   240

Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val Pro
            245   250   255

Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His Leu
            260   265   270

Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe
        275   280   285

Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu
        290   295   300

Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys
305   310   315   320

44

Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr
            325   330   335

Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu
            340   345   350

Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser
            355   360   365

Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro
    370   375   380

Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg
385   390   395   400

Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys
            405   410   415

Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile
            420   425   430

Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu
            435   440   445

Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser
    450   455   460

Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly
465   470   475   480

His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met
            485   490   495

Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr
            500   505   510

Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn
            515   520   525

Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr
            530   535   540

Ala Glu Arg Pro Pro Ala Asp Leu Ala Val
545   550

45

<210> 18
<211> 549
<212> PRT
<213> Ustilago maydis

<220>
<221> MISC_FEATURE
<222> (1)..(549)
<223> N-terminal deleted Ustilago ACCase BC domain (AAs 12-560)

<400> 18

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Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala
1               5                   10                  15


Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu
            20                  25                  30


Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg
            35                  40                  45


Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr
    50                  55                  60


Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg
65                  70                  75                  80


Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn
                85                  90                  95


Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val
                100                 105                 110


His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu
            115                 120                 125


Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro
    130                 135                 140


Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile
145                 150                 155                 160


Val Ala Gln His Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly
                165                 170                 175


Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp
                180                 185                 190
```

46

Asp Val Tyr Gln Gln Ala Cys Ile His Thr Ala Glu Glu Gly Leu Glu
        195   200   205

Lys Ala Glu Lys Ile Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly
        210   215   220

Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys
225   230   235   240

Gln Leu Tyr Asn Ala Val Leu Gly Glu Val Pro Gly Ser Pro Val Phe
            245   250   255

Val Met Lys Leu Ala Gly Gln Ala Arg His Leu Glu Val Gln Leu Leu
            260   265   270

Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser
            275   280   285

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile
    290   295   300

Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys Ala Ala Val Arg Leu
305   310   315   320

Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr
            325   330   335

Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu
            340   345   350

Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro
            355   360   365

Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg
        370   375   380

Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile
385   390   395   400

Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro
            405   410   415

Gln Pro Gln Gly His Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro
            420   425   430

Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe

Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly
    450   455   460

Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr
465   470   475   480

Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys
            485   490   495

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile
            500   505   510

Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly
        515   520   525

Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro
    530   535   540

Ala Asp Leu Ala Val
545

<210> 19
<211> 539
<212> PRT
<213> Ustilago maydis

<220>
<221> MISC_FEATURE
<222> (1)..(539)
<223> N-terminal deleted Ustilago ACCse BC domain (AAs 22-560)

<400> 19

Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser
1   5   10   15

Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys
            20   25   30

Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu
        35   40   45

Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val
    50   55   60

Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly

Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val
            85   90   95

Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala
            100   105   110

Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys
            115   120   125

Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp
    130   135   140

Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met
145   150   155   160

Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly
                165   170   175

Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr
            180   185   190

Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met
            195   200   205

Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr
    210   215   220

Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val
225   230   235   240

Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His
                245   250   255

Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile
            260   265   270

Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu
            275   280   285

Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu
            290   295   300

Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly
305   310   315   320

Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu
                ·325   330   335

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val
            340   345   350

Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile
        355   360   365

Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro
    370   375   380

Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe
385   390   395   400

Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg
            405   410   415

Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala
            420   425   430

Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe
        435   440   445

Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe
    450   455   460

Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln
465   470   475   480

Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr
            485   490   495

Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser
            500   505   510

Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu
        515   520   525

Thr Ala Glu Arg Pro Pro Ala Asp Leu Ala Val
    530   535

<210>   20
<211>   529
<212>   PRT

<213> Ustilago maydis

<220>
<221> MISC_FEATURE
<222> (1)..(529)
<223> N-terminal deleted Ustilago ACCase BC domain (AAs 32-560)

<400> 20

Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn
1   5   10   15

Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr
            20   25   30

Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr
            35   40   45

Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln
        50   55   60

Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val
65   70   75   80

Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp
                85   90   95

Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu
            100   105   110

Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala
            115   120   125

Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His
        130   135   140

Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr
145   150   155   160

Met Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln
                165   170   175

Gln Ala Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys
                180   185   190

Ile Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys
        195   200   205

```
Gly Ile Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn
    210             215             220

Ala Val Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu
225             230             235                 240

Ala Gly Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr
            245             250             255

Gly Asn Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg
            260             265             270

His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp
            275             280             285

Ala Arg Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val
    290             295             300

Gly Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser
305             310             315                 320

Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His
            325             330             335

Pro Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu
            340             345             350

Gln Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr
            355             360             365

Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe
    370             375             380

Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly
385             390             395                 400

His Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe
            405             410             415

Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr
            420             425             430

Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu
            435             440             445
```

52

Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg
    450   455   460

Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile
465   470   475   480

Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu
                485   490   495

Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly
                500   505   510

Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro Ala Asp Leu Ala
        515   520   525

Val

<210> 21
<211> 519
<212> PRT
<213> Ustilago maydis

<220>
<221> MISC_FEATURE
<222> (1)..(519)
<223> N-terminal deleted Ustilago ACCase BC domain (AAs 42-560)

<400> 21

Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser
1   5   10   15

Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu
            20   25   30

Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr
        35   40   45

Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn
    50   55   60

Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala
65   70   75   80

Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro
            85   90   95

Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile Ile Phe Ile
                100   105   110

Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser
                115   120   125

Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met Pro Trp Ser Gly
    130   135   140

Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe Leu Thr Val
145   150   155   160

Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr Ala Glu Glu Gly
                165   170   175

Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met Ile Lys Ala Ser
                180   185   190

Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr Asn Gly Glu Glu
                195   200   205

Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val Pro Gly Ser Pro
    210   215   220

Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His Leu Glu Val Gln
225   230   235   240

Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe Gly Arg Asp
                245   250   255

Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val
                260   265   270

Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys Ala Ala Val
    275   280   285

Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Trp
    290   295   300

Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro
305   310   315   320

Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn
                325   330   335

Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu Tyr Ser

54

Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu
     355   360   365

Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg
     370   375   380

Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile Thr Ala Glu
385   390   395   400

Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu
            405   410   415

Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr
            420   425   430

Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe
            435   440   445

Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser
     450   455   460

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr
465   470   475   480

Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr
            485   490   495

Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg
            500   505   510

Pro Pro Ala Asp Leu Ala Val
            515

<210> 22
<211> 554
<212> PRT
<213> Ustilago maydis

<220>
<221> MISC_FEATURE
<222> (1)..(554)
<223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-555)

<400> 22

Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro

```
1                    5                           10                              15

Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln
            20              25                      30

Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile
            35              40                      45

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr
    50              55                      60

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu
65              70                      75                      80

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val
                85                      90                      95

Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu
            100                 105                 110

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly
        115                 120                 125

Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala
    130                 135                 140

Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg
145                 150                 155                 160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp
                165                 170                 175

Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met
            180                 185                 190

Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala
            195                 200                 205

Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly
    210                 215                 220

Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
225                 230                 235                 240

Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val
                245                 250                 255
```

Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly
          260   265   270

Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn
          275   280   285

Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
          290   295   300

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg
305   310   315   320

Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr
          325   330   335

Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu
          340   345   350

Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
          355   360   365

Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val
          370   375   380

Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr
385   390   395   400

Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser
          405   410   415

Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val
          420   425   430

Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro
          435   440   445

Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr
          450   455   460

Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala
465   470   475   480

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu
          485   490   495

57

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly
            500   505   510

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp
            515   520   525

Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile
            530   535   540

Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro
545   550

<210>   23
<211>   549
<212>   PRT
<213>   Ustilago maydis

<220>
<221>   MISC_FEATURE
<222>   (1)..(549)
<223>   C-terminal deleted Ustilago ACCase BC domain (AAs 2-550)

<400>   23

Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro
1   5   10   15

Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln
            20   25   30

Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile
            35   40   45

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr
            50   55   60

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu
65   70   75   80

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val
            85   90   95

Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu
            100   105   110

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly
            115   120   125

58

Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala
    130   135   140

Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg
145   150   155   160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp
                165   170   175

Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met
            180   185   190

Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala
            195   200   205

Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly
    210   215   220

Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
225   230   235   240

Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val
            245   250   255

Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly
            260   265   270

Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn
        275   280   285

Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
    290   295   300

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg
305   310   315   320

Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr
            325   330   335

Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu
            340   345   350

Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
    355   360   365

```
Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val
    370                 375             380

Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr
385                 390             395                 400

Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser
            405             410             415

Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val
            420             425             430

Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro
        435             440             445

Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr
    450             455             460

Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala
465             470             475                 480

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu
            485             490             495

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly
        500             505             510

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp
        515             520             525

Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile
    530             535             540

Gln Asp Arg Leu Thr
545


<210>  24
<211>  539
<212>  PRT
<213>  Ustilago maydis


<220>
<221>  MISC_FEATURE
<222>  (1)..(539)
<223>  C-terminal deleted Ustilago ACCase BC domain (AAs 2-540)

<400>  24
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```
Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro
1               5                   10                  15

Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln
                20                  25                  30

Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile
            35                  40                  45

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr
        50                  55                  60

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu
65                  70                  75                  80

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val
                85                  90                  95

Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu
            100                 105                 110

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly
        115                 120                 125

Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala
    130                 135                 140

Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg
145                 150                 155                 160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp
                165                 170                 175

Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met
            180                 185                 190

Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala
        195                 200                 205

Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly
    210                 215                 220

Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
225                 230                 235                 240

Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val
```

61

Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly
            260   265   270

Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn
        275   280   285

Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
    290   295   300

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg
305   310   315   320

Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr
            325   330   335

Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu
            340   345   350

Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
        355   360   365

Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val
    370   375   380

Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr
385   390   395   400

Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser
            405   410   415

Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val
            420   425   430

Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro
        435   440   445

Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr
    450   455   460

Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala
465   470   475   480

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu
            485   490   495

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly
        500   505   510

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp
        515   520   525

Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp
    530   535

<210> 25
<211> 529
<212> PRT
<213> Ustilago maydis

<220>
<221> MISC_FEATURE
<222> (1)..(529)
<223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-530)

<400> 25

Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro
1   5   10   15

Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln
        20   25   30

Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile
        35   40   45

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr
    50   55   60

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu
65   70   75   80

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val
                85   90   95

Glu Val Pro Gly Gly Ser Asn Asn Asn Tyr Ala Asn Val Asp Leu
            100   105   110

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly
            115   120   125

Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala
    130   135   140

63

Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg
145   150   155   160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp
            165   170   175

Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met
            180   185   190

Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala
            195   200   205

Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly
    210   215   220

Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
225   230   235   240

Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val
            245   250   255

Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly
            260   265   270

Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn
            275   280   285

Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
    290   295   300

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg
305   310   315   320

Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr
            325   330   335

Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu
            340   345   350

Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
            355   360   365

Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val
370   375   380

64

```
Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr
385             390             395                     400


Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser
            405             410             415


Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val
            420             425             430


Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro
        435             440             445


Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr
        450             455             460


Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala
465             470             475             480


Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu
            485             490             495


Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly
        500             505             510


Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp
        515             520             525


Ala


<210>  26
<211>  519
<212>  PRT
<213>  Ustilago maydis


<220>
<221>  MISC_FEATURE
<222>  (1)..(519)
<223>  C-terminal deleted Ustilago ACCase BC domain (AAs2-520)


<400>  26


Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro
1               5               10                      15


Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln
                20              25              30
```

```
Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile
        35                  40                  45

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr
    50                  55                  60

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu
65                  70                  75                  80

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val
                85                  90                  95

Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu
            100                 105                 110

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly
        115                 120                 125

Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala
    130                 135                 140

Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg
145                 150                 155                 160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp
            165                 170                 175

Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met
        180                 185                 190

Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala
        195                 200                 205

Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly
    210                 215                 220

Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
225                 230                 235                 240

Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val
            245                 250                 255

Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly
            260                 265                 270
```

66

```
Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn
        275             280             285

Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
    290             295             300

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg
305             310             315             320

Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr
            325             330             335

Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu
        340             345             350

Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
        355             360             365

Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val
    370             375             380

Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr
385             390             395             400

Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser
            405             410             415

Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val
            420             425             430

Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro
        435             440             445

Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr
    450             455             460

Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala
465             470             475             480

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu
            485             490             495

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly
            500             505             510

Asp Phe Arg Thr Thr Val Glu
```

515

<210> 27
<211> 554
<212> PRT
<213> Ustilago maydis

<220>
<221> MISC_FEATURE
<222> (1)..(554)
<223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 4-547)

<400> 27

Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu
1   5   10   15

Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly
            20   25   30

His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala
        35   40   45

Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly
    50   55   60

Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu
65   70   75   80

Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val
                85   90   95

Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val
                100   105   110

Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly
            115   120   125

His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys
        130   135   140

His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu
145   150   155   160

Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro
                165   170   175

Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp

68

Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile
        195   200   205

His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro
    210   215   220

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys
225   230   235   240

Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly
            245   250   255

Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala
            260   265   270

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile
        275   280   285

Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile
    290   295   300

Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser
305   310   315   320

Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser
            325   330   335

Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala
            340   345   350

Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu
        355   360   365

Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met
    370   375   380

Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met
385   390   395   400

Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu
            405   410   415

Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala
        420   425   430

```
Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met
        435                 440                 445


Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly
        450                 455                 460


Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser
465                 470                 475                 480


Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg
                485                 490                 495


Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe
                500                 505                 510


Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe
        515                 520                 525


Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp
        530                 535                 540


Arg Leu Thr Ala Glu Arg Pro Pro Ala Asp
545                 550


<210>    28
<211>    549
<212>    PRT
<213>    Ustilago maydis


<220>
<221>    MISC_FEATURE
<222>    (1)..(549)
<223>    N- and C-terminal deleted Ustilago ACCase BC domain (AAs 7-555)


<400>    28

Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro
1                 5                 10                  15


Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val
                20                  25                  30


Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu
        35                  40                  45


Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg
        50                  55                  60
```

70

Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn
65   70   75   80

Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly
             85   90   95

Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala
             100   105   110

Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser
         115   120   125

Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile
    130   135   140

Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys
145   150   155   160

Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met Pro
             165   170   175

Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe
             180   185   190

Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr Ala
         195   200   205

Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met Ile
    210   215   220

Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr Asn
225   230   235   240

Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val Pro
             245   250   255

Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His Leu
             260   265   270

Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe
         275   280   285

Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu
    290   295   300

71

Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys
305   310   315   320

Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr
                325   330   335

Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu
                340   345   350

Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser
                355   360   365

Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro
        370   375   380

Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg
385   390   395   400

Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys
                405   410   415

Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile
                420   425   430

Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu
                435   440   445

Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser
        450   455   460

Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly
465   470   475   480

His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met
                485   490   495

Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr
                500   505   510

Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn
        515   520   525

Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr
        530   535   540

72

Ala Glu Arg Pro Pro
545

<210> 29
<211> 539
<212> PRT
<213> Ustilago maydis

<220>
<221> MISC_FEATURE
<222> (1)..(539)
<223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 12-550)

<400> 29

Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala
1   5   10   15

Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu
            20   25   30

Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg
        35   40   45

Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr
    50   55   60

Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg
65   70   75   80

Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn
                85   90   95

Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val
                100   105   110

His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu
            115   120   125

Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro
        130   135   140

Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile
145   150   155   160

Val Ala Gln His Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly
                165   170   175

```
Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp
        180             185                 190

Asp Val Tyr Gln Gln Ala Cys Ile His Thr Ala Glu Glu Gly Leu Glu
        195             200                 205

Lys Ala Glu Lys Ile Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly
    210             215                 220

Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys
225                 230                 235                     240

Gln Leu Tyr Asn Ala Val Leu Gly Glu Val Pro Gly Ser Pro Val Phe
            245             250                 255

Val Met Lys Leu Ala Gly Gln Ala Arg His Leu Glu Val Gln Leu Leu
            260             265                 270

Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser
        275             280                 285

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile
    290             295                 300

Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys Ala Ala Val Arg Leu
305             310                 315                     320

Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr
            325             330                 335

Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu
        340             345                 350

Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro
        355             360                 365

Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg
    370             375                 380

Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile
385             390                 395                     400

Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro
            405             410                 415

Gln Pro Gln Gly His Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro
```

```
Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe
        435             440             445


Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly
        450             455             460


Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr
465             470             475             480


Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys
                485             490             495


Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile
            500             505             510


Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly
        515             520             525


Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr
    530             535
```

<210> 30
<211> 529
<212> PRT
<213> Ustilago maydis

<220>
<221> MISC_FEATURE
<222> (1)..(529)
<223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 17-545)

<400> 30

```
Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys
1               5               10              15


Gln Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly
            20              25              30


Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu
        35              40              45


Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro
    50              55              60


Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr
```

Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp
            85   90   95

Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala
            100   105   110

Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala
            115   120   125

Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met
    130   135   140

Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala
145   150   155   160

Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met
            165   170   175

Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln
            180   185   190

Ala Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile
    195   200   205

Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly
    210   215   220

Ile Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala
225   230   235   240

Val Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala
            245   250   255

Gly Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly
            260   265   270

Asn Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His
            275   280   285

Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala
    290   295   300

Arg Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly
305   310   315   320

76

```
Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly
                325             330             335


Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro
            340             345             350


Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln
            355             360             365


Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu
        370             375             380


Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser
385             390             395             400


Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His
                405             410             415


Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys
            420             425             430


Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser
        435             440             445


Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr
    450             455             460


Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser
465             470             475             480


Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg
            485             490             495


Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr
            500             505             510


Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu
            515             520             525


Ile


<210>  31
<211>  519
<212>  PRT
```

<213>   Ustilago maydis

<220>
<221>   MISC_FEATURE
<222>   (1)..(519)
<223>   N- and C-terminal deleted Ustilago ACCase BC domain (AAs 22-540)

<400>   31

Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser
1   5   10   15

Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys
            20   25   30

Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu
        35   40   45

Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val
    50   55   60

Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly
65   70   75   80

Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val
            85   90   95

Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala
            100   105   110

Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys
        115   120   125

Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp
    130   135   140

Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met
145   150   155   160

Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly
            165   170   175

Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr
            180   185   190

Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met
    195   200   205

78

```
Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr
    210                     215             220

Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val
225                 230             235                     240

Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His
                245             250                     255

Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile
                260             265                 270

Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu
        275             280             285

Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu
    290             295             300

Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly
305             310             315                     320

Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu
            325             330                     335

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val
            340             345                 350

Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile
        355             360             365

Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro
    370             375             380

Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe
385             390             395                     400

Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg
            405             410                     415

Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala
        420             425                 430

Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe
    435             440                 445
```

Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe
    450   455   460

Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln
465   470   475   480

Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr
            485   490   495

Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser
            500   505   510

Asn Lys Ile Thr Thr Gly Trp
        515

<210>   32
<211>   580
<212>   PRT
<213>   Saccharomyces cerevisiae

<220>
<221>   MISC_FEATURE
<222>   (76)..(76)
<223>   Saccharomyces cerevisiae ACCase BC domain S77Y mutation

<400>   32

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1   5   10   15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile
            20   25   30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe
        35   40   45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala
    50   55   60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Tyr Val Arg Lys Trp
65   70   75   80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met
            85   90   95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala
            100   105   110

80

```
Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala
        115             120             125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala
        130             135             140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu
145             150             155             160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly
            165             170             175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala
            180             185             190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp
        195             200             205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp
    210             215             220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys
225             230             235             240

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly
            245             250             255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala
            260             265             270

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile
        275             280             285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala
    290             295             300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val
305             310             315             320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala
            325             330             335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly
            340             345             350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser
```

355   360   365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln
        370   375   380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala
385   390   395   400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp
                405   410   415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp
                420   425   430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile
        435   440   445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn
        450   455   460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg
465   470   475   480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn
                485   490   495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly
                500   505   510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu
        515   520   525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
        530   535   540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp
545   550   555   560

Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro
                565   570   575

Thr Leu Ala Val
            580

<210>   33
<211>   575

82

<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(575)
<223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 7-581)

<400> 33

```
Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser
1               5               10              15


Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val
            20              25              30


Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly
        35              40              45


Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala
    50              55              60


Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe
65              70              75              80


Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp
            85              90              95


Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu
            100             105             110


Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile
            115             120             125


Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp
    130             135             140


Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser
145             150             155             160


Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser
            165             170             175


Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val
            180             185             190


Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp
```

83

Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly
    210   215   220

Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly
225   230   235   240

Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
             245   250   255

Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala
             260   265   270

Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly
             275   280   285

Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr
    290   295   300

Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
305   310   315   320

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe
             325   330   335

His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr
             340   345   350

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys
             355   360   365

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
    370   375   380

Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile
385   390   395   400

Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr
             405   410   415

Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr
             420   425   430

Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys
    435   440   445

```
Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro
    450             455             460

Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val
465             470             475             480

Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser
                485             490             495

Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala
                500             505             510

Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly
        515             520             525

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu
    530             535             540

Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile
545             550             555             560

Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val
                565             570             575
```

<210> 34
<211> 570
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(570)
<223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs
      12-581)

<400> 34

```
Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu
1               5               10              15

Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu
                20              25              30

Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile
        35              40              45

Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile
```

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr
65   70   75   80

Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala
                85   90   95

Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr
            100   105   110

Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu
        115   120   125

Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu
    130   135   140

Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile
145   150   155   160

Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile
            165   170   175

Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp
            180   185   190

Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu
            195   200   205

Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro
    210   215   220

Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile
225   230   235   240

Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg
            245   250   255

Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro
            260   265   270

Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu
            275   280   285

Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe
            290   295   300

Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu
305   310   315   320

Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu Met Glu Lys
                325   330   335

Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser Ala Gly Thr
                340   345   350

Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu
                355   360   365

Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser
        370   375   380

Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro
385   390   395   400

Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His
                405   410   415

Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys
                420   425   430

Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile
                435   440   445

Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu
        450   455   460

His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser
465   470   475   480

Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly
                485   490   495

His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met
                500   505   510

Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr
                515   520   525

Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn
        530   535   540

Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr
545   550   555   560

Ala Glu Lys Pro Asp Pro Thr Leu Ala Val
                565   570

<210>   35
<211>   560
<212>   PRT
<213>   Saccharomyces cerevisiae

<220>
<221>   MISC_FEATURE
<222>   (1)..(560)
<223>   N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs
        22-581)

<400>   35

Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr
1   5   10   15

Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His
            20   25   30

Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile
        35   40   45

Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr
    50   55   60

Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu
65   70   75   80

Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile
            85   90   95

Glu Val Pro Gly Gly Thr Asn Asn Asn Tyr Ala Asn Val Asp Leu
            100   105   110

Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly
        115   120   125

Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln
    130   135   140

Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg
145   150   155   160

```
Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys
            165             170             175

Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val
            180             185             190

Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys
            195             200             205

Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile
    210             215             220

Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly
225             230             235             240

Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln
            245             250             255

Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala
            260             265             270

Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly
    275             280             285

Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His
    290             295             300

Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr
305             310             315             320

Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly
            325             330             335

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly
            340             345             350

Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro
    355             360             365

Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln
    370             375             380

Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu
385             390             395             400
```

```
Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys
                405             410                 415

Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His
            420             425                 430

Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys
            435             440                 445

Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn
    450             455                 460

Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe
465             470                 475                 480

Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln
            485                 490                 495

Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg
            500                 505                 510

Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr
        515             520                 525

Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu
    530             535                 540

Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val
545             550                 555                 560


<210>  36
<211>  550
<212>  PRT
<213>  Saccharomyces cerevisiae


<220>
<221>  MISC_FEATURE
<222>  (1)..(550)
<223>  N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs
       32-581


<400>  36

Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg
1               5                   10                  15


Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu
            20              25                  30
```

```
Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg
        35              40              45

Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val
    50              55              60

Ala Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg
65              70              75              80

Met Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn
            85              90              95

Tyr Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val
            100             105             110

Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu
        115             120             125

Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro
    130             135             140

Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile
145             150             155             160

Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly
            165             170             175

Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp
            180             185             190

Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu
        195             200             205

Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu
    210             215             220

Gly Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe
225             230             235             240

Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile
            245             250             255

Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu
        260             265             270
```

91

Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys
        275   280   285

Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr
        290   295   300

Ile Ala Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg
305   310   315   320

Leu Gly Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu
                325   330   335

Tyr Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg
                340   345   350

Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu
        355   360   365

Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile
        370   375   380

Ser Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu
385   390   395   400

Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg
                405   410   415

Pro Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp
                420   425   430

Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn
        435   440   445

Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn
        450   455   460

Gly Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala
465   470   475   480

Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu
                485   490   495

Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu
                500   505   510

Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr
        515   520   525

Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro
        530   535   540

Asp Pro Thr Leu Ala Val
545   550

<210> 37
<211> 540
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(540)
<223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs
      42-581)

<400> 37

Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr
1   5   10   15

Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
                20   25   30

Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp
        35   40   45

Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu Ala
        50   55   60

Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro Gly
65   70   75   80

Gly Thr Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile
                85   90   95

Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala
                100   105   110

Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys
        115   120   125

Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp
        130   135   140

93

Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys Ile
145   150   155   160

Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys Thr
                165   170   175

Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr
                180   185   190

Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro Val
            195   200   205

Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Gln Val
        210   215   220

Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn Glu
225   230   235   240

Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala Arg
                245   250   255

His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser
            260   265   270

Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile
        275   280   285

Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu Met
    290   295   300

Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser Ala
305   310   315   320

Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr Phe
            325   330   335

Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met
            340   345   350

Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly
        355   360   365

Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met Asn
    370   375   380

Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala
385   390   395   400

Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala Cys
            405   410   415

Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly
            420   425   430

Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr
            435   440   445

Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser Gln
    450   455   460

Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys
465   470   475   480

His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg
            485   490   495

Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu
            500   505   510

Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His Lys
            515   520   525

Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val
    530   535   540

<210>   38
<211>   575
<212>   PRT
<213>   Saccharomyces cerevisiae

<220>
<221>   MISC_FEATURE
<222>   (1)..(575)
<223>   C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs
        2-576)

<400>   38

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1   5   10   15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile
            20   25   30

```
Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe
        35                  40              45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala
        50              55              60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp
65              70              75                      80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met
            85              90                      95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala
            100             105             110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala
        115             120             125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala
        130             135             140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu
145             150             155             160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly
            165             170             175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala
            180             185             190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp
        195             200             205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp
        210             215             220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys
225             230             235             240

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly
            245             250             255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala
        260             265             270
```

96

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile
        275   280   285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala
    290   295   300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val
305   310   315   320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala
                325   330   335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly
            340   345   350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser
        355   360   365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln
    370   375   380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala
385   390   395   400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp
            405   410   415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp
        420   425   430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile
        435   440   445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn
    450   455   460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg
465   470   475   480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn
            485   490   495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly
            500   505   510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu

                                97

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
    530   535   540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp
545   550   555   560

Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp
            565   570   575

<210> 39
<211> 570
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(570)
<223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 2-571)

<400> 39

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1   5   10   15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile
            20   25   30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe
        35   40   45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala
    50   55   60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp
65   70   75   80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met
            85   90   95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala
            100   105   110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Tyr Ala
        115   120   125

98

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala
    130   135   140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu
145   150   155   160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly
                165   170   175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala
            180   185   190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp
        195   200   205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp
    210   215   220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys
225   230   235   240

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly
            245   250   255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala
            260   265   270

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile
        275   280   285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala
    290   295   300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val
305   310   315   320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala
                325   330   335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly
            340   345   350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser
        355   360   365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala
385   390   395   400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp
                405   410   415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp
                420   425   430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile
                435   440   445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn
        450   455   460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg
465   470   475   480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn
                485   490   495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly
                500   505   510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu
        515   520   525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
        530   535   540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp
545   550   555   560

Leu Asp Asp Leu Ile Thr His Lys Met Thr
                565   570

<210> 40
<211> 560
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(560)
<223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs

2-561)

<400> 40

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1   5   10   15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile
            20   25   30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe
        35   40   45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala
    50   55   60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp
65   70   75   80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met
            85   90   95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala
            100   105   110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala
        115   120   125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala
        130   135   140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu
145   150   155   160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly
            165   170   175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala
            180   185   190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp
        195   200   205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp
        210   215   220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys

101

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly
              245   250   255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala
              260   265   270

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile
          275   280   285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala
      290   295   300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val
305   310   315   320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala
              325   330   335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly
              340   345   350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser
          355   360   365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln
      370   375   380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala
385   390   395   400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp
              405   410   415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp
          420   425   430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile
          435   440   445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn
      450   455   460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg
465   470   475   480

```
Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn
                485             490             495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly
            500             505             510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu
        515             520             525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
    530             535             540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp
545             550             555             560


<210>  41
<211>  550
<212>  PRT
<213>  Saccharomyces cerevisiae


<220>
<221>  MISC_FEATURE
<222>  (1)..(550)
<223>  C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs
       2-551)

<400>  41

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1               5               10              15


Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile
            20              25              30


Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe
        35              40              45


Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala
    50              55              60


Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp
65              70              75              80


Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met
            85              90              95


Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala
```

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Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala
        115   120   125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala
        130   135   140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu
145   150   155   160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly
                165   170   175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala
            180   185   190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp
        195   200   205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp
        210   215   220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys
225   230   235   240

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly
                245   250   255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala
            260   265   270

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile
        275   280   285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala
    290   295   300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val
305   310   315   320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala
                325   330   335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly
            340   345   350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser
            355   360   365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln
            370   375   380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala
385   390   395   400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp
                405   410   415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp
            420   425   430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile
            435   440   445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn
    450   455   460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg
465   470   475   480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn
                485   490   495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly
                500   505   510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu
            515   520   525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
    530   535   540

Leu Leu Glu Thr Glu Asp
545   550

<210>   42
<211>   540
<212>   PRT
<213>   Saccharomyces cerevisiae

<220>

<221> MISC_FEATURE
<222> (1)..(540)
<223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs
      2-541)

<400> 42

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1   5   10   15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile
            20   25   30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe
            35   40   45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala
        50   55   60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp
65   70   75   80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met
                85   90   95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala
            100   105   110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala
            115   120   125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala
        130   135   140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu
145   150   155   160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly
                165   170   175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala
            180   185   190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp
        195   200   205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp
    210   215   220

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```
Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys
225                 230             235                 240

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly
                245             250                 255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala
            260             265             270

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile
        275             280             285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala
    290             295             300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val
305             310             315                 320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala
            325             330                 335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly
            340             345                 350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser
        355             360             365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln
    370             375             380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala
385             390             395                 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp
            405             410                 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp
            420             425                 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile
        435             440             445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn
    450             455             460
```

107

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg
465   470   475   480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn
                485   490   495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly
            500   505   510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu
            515   520   525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu
        530   535   540

<210> 43
<211> 575
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(575)
<223> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
      domain (AAs 4-578)

<400> 43

Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr
1   5   10   15

Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu
            20   25   30

Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys
        35   40   45

Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn
    50   55   60

Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr
65   70   75   80

Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr
                85   90   95

Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln
            100   105   110

108

Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val
        115   120   125

Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp
    130   135   140

Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu
145   150   155   160

Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala
            165   170   175

Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser
        180   185   190

Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val
        195   200   205

His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr
    210   215   220

Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys
225   230   235   240

Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly
            245   250   255

Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr
        260   265   270

His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys
        275   280   285

Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln
    290   295   300

Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg
305   310   315   320

Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala
            325   330   335

Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu
        340   345   350

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Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp
        355   360   365

Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu
        370   375   380

His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln
385   390   395   400

Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg
                405   410   415

Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu
                420   425   430

Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys
        435   440   445

Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly
        450   455   460

Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser
465   470   475   480

Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His
                485   490   495

Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn
                500   505   510

Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser
        515   520   525

Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu
        530   535   540

Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp
545   550   555   560

Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr
                565   570   575

<210> 44
<211> 570
<212> PRT
<213> Saccharomyces cerevisiae

110

<220>
<221>   MISC_FEATURE
<222>   (1)..(570)
<223>   N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
         domain (AAs 7-576)

<400>   44

Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser
1   5   10   15

Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val
            20   25   30

Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly
            35   40   45

Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala
        50   55   60

Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe
65   70   75   80

Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp
            85   90   95

Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu
            100   105   110

Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile
            115   120   125

Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp
        130   135   140

Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser
145   150   155   160

Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser
                165   170   175

Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val
            180   185   190

Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp
            195   200   205

```
Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly
    210             215             220

Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly
225             230             235             240

Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile
            245             250             255

Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala
            260             265             270

Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly
        275             280             285

Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr
    290             295             300

Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
305             310             315             320

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe
            325             330             335

His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr
            340             345             350

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys
        355             360             365

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
    370             375             380

Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile
385             390             395             400

Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr
            405             410             415

Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr
            420             425             430

Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys
    435             440             445
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Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro
    450   455   460

Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val
465   470   475   480

Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser
                485   490   495

Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala
                500   505   510

Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly
            515   520   525

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu
    530   535   540

Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile
545   550   555   560

Thr His Lys Met Thr Ala Glu Lys Pro Asp
                565   570

<210>   45
<211>   560
<212>   PRT
<213>   Saccharomyces cerevisiae

<220>
<221>   MISC_FEATURE
<222>   (1)..(560)
<223>   N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
         domain (AAs 12-571)

<400>   45

Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu
1   5   10   15

Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu
                20   25   30

Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile
            35   40   45

Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile
        50   55   60

113

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr
65   70   75   80

Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala
                85   90   95

Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr
            100   105   110

Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu
        115   120   125

Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu
    130   135   140

Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile
145   150   155   160

Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile
            165   170   175

Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp
        180   185   190

Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu
    195   200   205

Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro
210   215   220

Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile
225   230   235   240

Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg
            245   250   255

Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro
            260   265   270

Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu
        275   280   285

Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe
    290   295   300

Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu
305   310   315   320

Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu Met Glu Lys
                325   330   335

Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser Ala Gly Thr
                340   345   350

Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu
                355   360   365

Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser
        370   375   380

Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro
385   390   395   400

Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His
                405   410   415

Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys
                420   425   430

Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile
                435   440   445

Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu
        450   455   460

His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser
465   470   475   480

Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly
                485   490   495

His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met
                500   505   510

Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr
                515   520   525

Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn
        530   535   540

Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr

<210> 46
<211> 550
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(550)
<223> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
      domain (AAs 17-566)

<400> 46

Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe
1   5   10   15

Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp
            20   25   30

Phe Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile
            35   40   45

Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys
    50   55   60

Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala
65   70   75   80

Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met
                85   90   95

Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr
            100   105   110

Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp
            115   120   125

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro
    130   135   140

Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro
145   150   155   160

Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val
                165   170   175

```
Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val
            180                 185                 190

Asp Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp
        195                 200                 205

Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln
        210                 215                 220

Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly
225                 230                 235                 240

Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile
                245                 250                 255

Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe
            260                 265                 270

Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu
            275                 280                 285

Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser
    290                 295                 300

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile
305                 310                 315                 320

Ala Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu
            325                 330                 335

Gly Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr
            340                 345                 350

Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu
            355                 360                 365

Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro
    370                 375                 380

Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser
385                 390                 395                 400

Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile
            405                 410                 415

Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro
```

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                    420                    425                    430

        Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro
                435                440                445

        Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe
                450                455                460

        Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly
        465                470                475                480

        Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe
                        485                490                495

        Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys
                        500                505                510

        Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile
                515                520                525

        Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly
                530                535                540

        Trp Leu Asp Asp Leu Ile
        545                550


        <210>   47
        <211>   540
        <212>   PRT
        <213>   Saccharomyces cerevisiae


        <220>
        <221>   MISC_FEATURE
        <222>   (1)..(540)
        <223>   N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
                domain (AAs 22-561)

        <400>   47

        Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr
        1                5                10                15


        Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His
                        20                25                30


        Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile
                35                40                45
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```
Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr
    50              55              60

Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu
65              70              75                  80

Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile
                85              90                  95

Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu
            100             105             110

Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly
        115             120             125

Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln
    130             135             140

Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg
145             150             155             160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys
            165             170             175

Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val
        180             185             190

Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Ile Tyr Gln Lys
    195             200             205

Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile
    210             215             220

Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly
225             230             235             240

Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln
            245             250             255

Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala
            260             265             270

Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly
    275             280             285

Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His

                                119
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Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr
305   310   315   320

Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly
                        325   330   335

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly
                        340   345   350

Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro
                        355   360   365

Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln
            370   375   380

Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu
385   390   395   400

Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys
                        405   410   415

Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His
                        420   425   430

Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys
            435   440   445

Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn
    450   455   460

Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe
465   470   475   480

Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln
                        485   490   495

Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg
                        500   505   510

Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr
            515   520   525

Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp
    530   535   540

<210> 48
<211> 545
<212> PRT
<213> Phytophthora infestans

<220>
<221> MISC_FEATURE
<222> (1)..(545)
<223> N-terminal deleted Phytophthora ACCase BC domain (AAs 11-555)

<400> 48

Asp Val Ala Ala Tyr Ala Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn
1   5   10   15

Tyr Ala Ser Met Glu Glu Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro
                20   25   30

Ile Thr Ser Val Leu Ile Ala Asn Asn Gly Ile Ser Ala Val Lys Ala
                35   40   45

Ile Arg Ser Ile Arg Ser Trp Ser Tyr Glu Met Phe Ala Asp Glu His
        50   55   60

Val Val Thr Phe Val Val Met Ala Thr Pro Glu Asp Leu Lys Ala Asn
65   70   75   80

Ala Glu Tyr Ile Arg Met Ala Glu His Val Val Glu Val Pro Gly Gly
                85   90   95

Ser Asn Asn His Asn Tyr Ala Asn Val Ser Leu Ile Ile Glu Ile Ala
                100   105   110

Glu Arg Phe Asn Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser
        115   120   125

Glu Asn Pro Leu Leu Pro Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile
        130   135   140

Val Phe Ile Gly Pro Pro Gly Lys Pro Met Arg Ala Leu Gly Asp Lys
145   150   155   160

Ile Gly Ser Thr Ile Ile Ala Gln Ser Ala Lys Val Pro Thr Ile Ala
                165   170   175

Trp Asn Gly Asp Gly Met Glu Val Asp Tyr Lys Glu His Asp Gly Ile
                180   185   190

121

Pro Asp Glu Ile Tyr Asn Ala Ala Met Leu Arg Asp Gly Gln His Cys
        195   200   205

Leu Asp Glu Cys Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser
        210   215   220

Glu Gly Gly Gly Gly Lys Gly Ile Arg Met Val His Glu Glu Ser Gln
225   230   235   240

Val Leu Ser Ala Trp Glu Ala Val Arg Gly Glu Ile Pro Gly Ser Pro
                245   250   255

Ile Phe Val Met Lys Leu Ala Pro Lys Ser Arg His Leu Glu Val Gln
            260   265   270

Leu Leu Ala Asp Thr Tyr Gly Asn Ala Ile Ala Leu Ser Gly Arg Asp
        275   280   285

Cys Ser Val Gln Arg Arg His Gln Lys Ile Val Glu Glu Gly Pro Val
    290   295   300

Leu Ala Pro Thr Gln Glu Val Trp Glu Lys Met Met Arg Ala Ala Thr
305   310   315   320

Arg Leu Ala Gln Glu Val Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr
                325   330   335

Leu Phe Ser Glu Leu Pro Glu Asp Asn Gly Asn Ser Phe Phe Phe Leu
            340   345   350

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Val Thr Glu Met Ile
        355   360   365

Thr His Val Asn Leu Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile
    370   375   380

Pro Leu His Cys Ile Pro Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala
385   390   395   400

Phe Glu Thr Thr Val Ile Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro
                405   410   415

His Gly His Val Ile Ala Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala
            420   425   430

122

Gly Phe Gln Pro Thr Ser Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser
        435   440   445

Thr Pro Asp Val Trp Gly Tyr Phe Ser Val Asp Ser Ser Gly Gln Val
    450   455   460

His Glu Phe Ala Asp Ser Gln Ile Gly His Leu Phe Ser Trp Ser Pro
465   470   475   480

Thr Arg Glu Lys Ala Arg Lys Asn Met Val Leu Ala Leu Lys Glu Leu
            485   490   495

Ser Ile Arg Gly Asp Ile His Thr Thr Val Glu Tyr Ile Val Asn Met
            500   505   510

Met Glu Ser Asp Asp Phe Lys Tyr Asn Arg Ile Ser Thr Ser Trp Leu
        515   520   525

Asp Glu Arg Ile Ser His His Asn Glu Val Arg Leu Gln Gly Arg Pro
    530   535   540

Asp
545

<210> 49
<211> 535
<212> PRT
<213> Phytophthora infestans

<220>
<221> MISC_FEATURE
<222> (1)..(535)
<223> N-terminal deleted Phytophthora ACCase BC domain (AAs 21-555)

<400> 49

Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu Tyr Val Arg Leu
1   5   10   15

Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile Ala Asn Asn Gly
            20   25   30

Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser Trp Ser Tyr Glu
        35   40   45

Met Phe Ala Asp Glu His Val Val Thr Phe Val Val Met Ala Thr Pro
    50   55   60

123

Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met Ala Glu His Val
65   70   75   80

Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr Ala Asn Val Ser
                85   90   95

Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp Ala Val Trp Ala
            100   105   110

Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Asp Thr Leu Ala
            115   120   125

Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro Gly Lys Pro Met
    130   135   140

Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile Ala Gln Ser Ala
145   150   155   160

Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met Glu Val Asp Tyr
                165   170   175

Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn Ala Ala Met Leu
            180   185   190

Arg Asp Gly Gln His Cys Leu Asp Glu Cys Lys Arg Ile Gly Phe Pro
            195   200   205

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Met
    210   215   220

Val His Glu Glu Ser Gln Val Leu Ser Ala Trp Glu Ala Val Arg Gly
225   230   235   240

Glu Ile Pro Gly Ser Pro Ile Phe Val Met Lys Leu Ala Pro Lys Ser
                245   250   255

Arg His Leu Glu Val Gln Leu Leu Ala Asp Thr Tyr Gly Asn Ala Ile
            260   265   270

Ala Leu Ser Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile
        275   280   285

Val Glu Glu Gly Pro Val Leu Ala Pro Thr Gln Glu Val Trp Glu Lys
    290   295   300

124

Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val Glu Tyr Val Asn
305   310   315   320

Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro Glu Asp Asn Gly
                325   330   335

Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His
            340   345   350

Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro Ala Ala Gln Leu
            355   360   365

Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro Asp Val Arg Arg
    370   375   380

Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile Asp Phe Asp Ala
385   390   395   400

Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala Ala Arg Ile Thr
            405   410   415

Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser Gly Ala Ile Gln
            420   425   430

Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly Tyr Phe Ser Val
            435   440   445

Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser Gln Ile Gly His
    450   455   460

Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg Lys Asn Met Val
465   470   475   480

Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile His Thr Thr Val
            485   490   495

Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe Lys Tyr Asn Arg
            500   505   510

Ile Ser Thr Ser Trp Leu Asp Glu Arg Ile Ser His His Asn Glu Val
    515   520   525

Arg Leu Gln Gly Arg Pro Asp
    530   535

<210> 50

<211> 545
<212> PRT
<213> Phytophthora infestans

<220>
<221> MISC_FEATURE
<222> (1)..(545)
<223> C-terminal deleted Phytophthora ACCase BC domain (AAs 1-545)

<400> 50

Met Val Ala Glu Glu Ala Pro Pro Ala Ala Asp Val Ala Ala Tyr Ala
1   5   10   15

Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu
            20   25   30

Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile
        35   40   45

Ala Asn Asn Gly Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser
    50   55   60

Trp Ser Tyr Glu Met Phe Ala Asp Glu His Val Val Thr Phe Val Val
65   70   75   80

Met Ala Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met
            85   90   95

Ala Glu His Val Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr
            100   105   110

Ala Asn Val Ser Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp
        115   120   125

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro
    130   135   140

Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro
145   150   155   160

Gly Lys Pro Met Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile
            165   170   175

Ala Gln Ser Ala Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met
            180   185   190

Glu Val Asp Tyr Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn

126

Ala Ala Met Leu Arg Asp Gly Gln His Cys Leu Asp Glu Cys Lys Arg
    210   215   220

Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys
225   230   235   240

Gly Ile Arg Met Val His Glu Glu Ser Gln Val Leu Ser Ala Trp Glu
            245   250   255

Ala Val Arg Gly Glu Ile Pro Gly Ser Pro Ile Phe Val Met Lys Leu
            260   265   270

Ala Pro Lys Ser Arg His Leu Glu Val Gln Leu Leu Ala Asp Thr Tyr
        275   280   285

Gly Asn Ala Ile Ala Leu Ser Gly Arg Asp Cys Ser Val Gln Arg Arg
    290   295   300

His Gln Lys Ile Val Glu Glu Gly Pro Val Leu Ala Pro Thr Gln Glu
305   310   315   320

Val Trp Glu Lys Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val
            325   330   335

Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro
            340   345   350

Glu Asp Asn Gly Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu
    355   360   365

Gln Val Glu His Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro
    370   375   380

Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro
385   390   395   400

Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile
            405   410   415

Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala
        420   425   430

Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser
        435   440   445

```
Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly
    450             455             460

Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser
465             470             475             480

Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg
            485             490             495

Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile
            500             505             510

His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe
            515             520             525

Lys Tyr Asn Arg Ile Ser Thr Ser Trp Leu Asp Glu Arg Ile Ser His
    530             535             540

His
545


<210>  51
<211>  535
<212>  PRT
<213>  Phytophthora infestans


<220>
<221>  MISC_FEATURE
<222>  (1)..(535)
<223>  C-terminal deleted Phytophthora ACCase BC domain (AAs 1-535)

<400>  51

Met Val Ala Glu Glu Ala Pro Pro Ala Ala Asp Val Ala Ala Tyr Ala
1               5               10              15

Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu
            20              25              30

Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile
            35              40              45

Ala Asn Asn Gly Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser
    50              55              60

Trp Ser Tyr Glu Met Phe Ala Asp Glu His Val Val Thr Phe Val Val
65              70              75              80
```

128

```
Met Ala Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met
            85              90                  95

Ala Glu His Val Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr
            100             105                 110

Ala Asn Val Ser Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp
            115             120                 125

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro
    130             135             140

Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro
145             150             155                 160

Gly Lys Pro Met Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile
            165             170             175

Ala Gln Ser Ala Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met
            180             185             190

Glu Val Asp Tyr Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn
    195             200             205

Ala Ala Met Leu Arg Asp Gly Gln His Cys Leu Asp Glu Cys Lys Arg
    210             215             220

Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys
225             230             235                 240

Gly Ile Arg Met Val His Glu Glu Ser Gln Val Leu Ser Ala Trp Glu
            245             250             255

Ala Val Arg Gly Glu Ile Pro Gly Ser Pro Ile Phe Val Met Lys Leu
            260             265             270

Ala Pro Lys Ser Arg His Leu Glu Val Gln Leu Leu Ala Asp Thr Tyr
            275             280             285

Gly Asn Ala Ile Ala Leu Ser Gly Arg Asp Cys Ser Val Gln Arg Arg
            290             295             300

His Gln Lys Ile Val Glu Glu Gly Pro Val Leu Ala Pro Thr Gln Glu
305             310             315                 320
```

129

```
Val Trp Glu Lys Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val
                325             330             335

Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro
            340             345             350

Glu Asp Asn Gly Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu
            355             360             365

Gln Val Glu His Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro
    370             375             380

Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro
385             390             395             400

Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile
            405             410             415

Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala
            420             425             430

Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser
            435             440             445

Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly
    450             455             460

Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser
465             470             475             480

Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg
            485             490             495

Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile
            500             505             510

His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe
            515             520             525

Lys Tyr Asn Arg Ile Ser Thr
    530             535


<210>   52
<211>   581
<212>   PRT
<213>   Magnaporthe grisea
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<220>
<221> MISC_FEATURE
<222> (1)..(581)
<223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 12-592

<400> 52

```
Asn Ser Ser Arg Gln Arg Asn Gly Ala Asn Gly Val Thr Val Pro Val
1               5                   10                  15


Ala Asn Gly Lys Ala Thr Tyr Ala Gln Arg His Lys Ile Ala Asp His
            20                  25                  30


Phe Ile Gly Gly Asn Arg Leu Glu Asn Ala Pro Pro Ser Lys Val Lys
            35                  40                  45


Glu Trp Val Ala Ala His Asp Gly His Thr Val Ile Thr Asn Val Leu
        50                  55                  60


Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg
65                  70                  75                  80


Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr
            85                  90                  95


Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg
            100                 105                 110


Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr Asn Asn Asn Asn
            115                 120                 125


Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu Arg Met Asn Val
    130                 135                 140


His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu
145                 150                 155                 160


Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro
            165                 170                 175


Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile
            180                 185                 190


Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp Ser Gly Thr Gly
    195                 200                 205
```

131

Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val Thr Val Asp Asp
210   215   220

Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln Glu Gly Leu Glu
225   230   235   240

Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly
                245   250   255

Gly Gly Gly Lys Gly Ile Arg Lys Ala Val Ser Glu Glu Gly Phe Glu
            260   265   270

Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly Ser Pro Ile Phe
        275   280   285

Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu Val Gln Leu Leu
    290   295   300

Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser
305   310   315   320

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile
            325   330   335

Ala Lys Pro Asp Thr Phe Lys Ala Met Glu Glu Ala Ala Val Arg Leu
            340   345   350

Gly Arg Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr
            355   360   365

Ser His Ala Asp Asp Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu
    370   375   380

Gln Val Glu His Pro Thr Thr Glu Gly Val Ser Gly Val Asn Leu Pro
385   390   395   400

Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu His Arg Ile Ser
                405   410   415

Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu Ser Thr Glu Ile
            420   425   430

Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro
        435   440   445

Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro

132

Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His Glu Leu Asn Phe
465   470   475   480

Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly
            485   490   495

Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Tyr
        500   505   510

Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val Ile Ala Leu Lys
        515   520   525

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile
    530   535   540

Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly
545   550   555   560

Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr Ala Glu Arg Pro Asp
            565   570   575

Lys Met Leu Ala Val
            580

<210> 53
<211> 571
<212> PRT
<213> Magnaporthe grisea

<220>
<221> MISC_FEATURE
<222> (1)..(571)
<223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 22-591)

<400> 53

Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr Tyr Ala Gln Arg
1   5   10   15

His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg Leu Glu Asn Ala
            20   25   30

Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His Asp Gly His Thr
        35   40   45

Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys

```
          50                      55                      60

Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu
65              70              75                      80

Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala
                85              90                      95

Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly
            100             105             110

Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val
        115             120             125

Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala
    130             135             140

Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys
145             150             155             160

Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp
            165             170             175

Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile
        180             185             190

Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly
        195             200             205

Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser
    210             215             220

Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met
225             230             235             240

Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Ala Val
            245             250             255

Ser Glu Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile
            260             265             270

Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His
        275             280             285

Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu
    290             295             300


                            134
```

Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu
305   310   315   320

Glu Ala Pro Val Thr Ile Ala Lys Pro Asp Thr Phe Lys Ala Met Glu
                325   330   335

Glu Ala Ala Val Arg Leu Gly Arg Leu Val Gly Tyr Val Ser Ala Gly
                340   345   350

Thr Val Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys Phe Tyr Phe Leu
                355   360   365

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Gly Val
        370   375   380

Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile
385   390   395   400

Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro
                405   410   415

Lys Leu Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu
                420   425   430

Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg
        435   440   445

Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val
        450   455   460

Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe
465   470   475   480

Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe
                485   490   495

Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His
                500   505   510

Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr
                515   520   525

Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu
        530   535   540

135

Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu
545   550   555   560

Thr Ala Glu Arg Pro Asp Lys Met Leu Ala Val
                565   570

<210> 54
<211> 581
<212> PRT
<213> Magnaporthe grisea

<220>
<221> MISC_FEATURE
<222> (1)..(581)
<223> C-terminal deleted Magnaporthe ACCase (AAs 2-582)

<400> 54

Thr Glu Thr Asn Gly Thr Ala Ala Ala Asn Ser Ser Arg Gln Arg
1   5   10   15

Asn Gly Ala Asn Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr
                20   25   30

Tyr Ala Gln Arg His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg
                35   40   45

Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His
      50   55   60

Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile
65   70   75   80

Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr
                85   90   95

Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu
                100   105   110

Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val
            115   120   125

Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu
        130   135   140

Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly
145   150   155   160

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala
            165   170   175

Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg
            180   185   190

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln
            195   200   205

Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile
    210   215   220

Asp Lys Lys Gly Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly
225   230   235   240

Cys Val Thr Ser Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly
            245   250   255

Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
            260   265   270

Arg Lys Ala Val Ser Glu Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala
    275   280   285

Ala Ser Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly
    290   295   300

Asn Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn
305   310   315   320

Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
            325   330   335

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Pro Asp Thr Phe
            340   345   350

Lys Ala Met Glu Glu Ala Ala Val Arg Leu Gly Arg Leu Val Gly Tyr
            355   360   365

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys
    370   375   380

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
385   390   395   400

137

```
Thr Glu Gly Val Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile
            405             410             415

Ala Met Gly Ile Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr
            420             425             430

Gly Val Asp Pro Lys Leu Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn
            435             440             445

Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu
    450             455             460

Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro
465             470             475             480

Ser Asn Gly Val Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val
            485             490             495

Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser
            500             505             510

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala
            515             520             525

Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly
    530             535             540

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu
545             550             555             560

Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile
            565             570             575

Ser Lys Lys Leu Thr
            580


<210>  55
<211>  571
<212>  PRT
<213>  Magnaporthe grisea


<220>
<221>  MISC_FEATURE
<222>  (1)..(571)
<223>  C-terminal deleted Magnaporthe ACCase BC domain (AAs 2-572)

<400>  55
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Thr Glu Thr Asn Gly Thr Ala Ala Ala Ala Asn Ser Ser Arg Gln Arg
1   5   10   15

Asn Gly Ala Asn Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr
            20   25   30

Tyr Ala Gln Arg His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg
        35   40   45

Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His
        50   55   60

Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile
65   70   75   80

Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr
            85   90   95

Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu
            100   105   110

Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val
        115   120   125

Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu
        130   135   140

Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly
145   150   155   160

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala
            165   170   175

Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg
            180   185   190

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln
        195   200   205

Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile
        210   215   220

Asp Lys Lys Gly Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly
225   230   235   240

Cys Val Thr Ser Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly

139

Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile
            260   265   270

Arg Lys Ala Val Ser Glu Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala
            275   280   285

Ala Ser Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly
    290   295   300

Asn Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn
305   310   315   320

Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln
                325   330   335

Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Pro Asp Thr Phe
            340   345   350

Lys Ala Met Glu Glu Ala Ala Val Arg Leu Gly Arg Leu Val Gly Tyr
            355   360   365

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys
    370   375   380

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr
385   390   395   400

Thr Glu Gly Val Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile
            405   410   415

Ala Met Gly Ile Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr
            420   425   430

Gly Val Asp Pro Lys Leu Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn
    435   440   445

Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu
    450   455   460

Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro
465   470   475   480

Ser Asn Gly Val Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val
            485   490   495

```
Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser
            500                 505                 510

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala
            515                 520                 525

Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly
            530                 535                 540

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu
545                 550                 555                 560

Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly Trp
                565                 570
```

<210> 56
<211> 622
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(622)
<223> C-terminal deleted Human ACCase1 BC domain (AAs 1-622)

<400> 56

```
Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His
1               5                   10                  15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
            20                  25                  30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
            35                  40                  45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
            50                  55                  60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser
65                  70                  75                  80

Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser
                85                  90                  95

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe
            100                 105                 110
```

141

Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile
        115   120   125

Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met
        130   135   140

Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu
145   150   155   160

Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val
            165   170   175

Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu
            180   185   190

Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly
        195   200   205

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys
    210   215   220

Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu
225   230   235   240

Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro
            245   250   255

Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn
            260   265   270

Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys
            275   280   285

Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val
    290   295   300

Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly
305   310   315   320

Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln
            325   330   335

Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala
        340   345   350

```
Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly
        355                 360             365

Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His
        370             375             380

Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val
385             390             395             400

Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly
                405             410             415

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser
            420             425             430

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys
        435             440             445

Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile
    450             455             460

Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr
465             470             475             480

Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala
            485             490             495

His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser
        500             505             510

Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu
        515             520             525

Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala
        530             535             540

Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys
545             550             555             560

Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val
            565             570             575

Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu
        580             585             590
```

Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile
        595   600   605

Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln
        610   615   620

<210> 57
<211> 612
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(612)
<223> C-terminal deleted Human ACCase1 BC domain (AAs 1-612)

<400> 57

Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His
1   5   10   15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu
            20   25   30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser
        35   40   45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile
    50   55   60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser
65   70   75   80

Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser
            85   90   95

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe
            100   105   110

Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile
            115   120   125

Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met
    130   135   140

Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu
145   150   155   160

144

Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val
165   170   175

Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu
180   185   190

Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly
195   200   205

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys
210   215   220

Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu
225   230   235   240

Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro
245   250   255

Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn
260   265   270

Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys
275   280   285

Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val
290   295   300

Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly
305   310   315   320

Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln
325   330   335

Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala
340   345   350

Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly
355   360   365

Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His
370   375   380

Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val
385   390   395   400

Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser
        420   425   430

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys
        435   440   445

Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile
    450   455   460

Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr
465   470   475   480

Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala
            485   490   495

His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser
        500   505   510

Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu
        515   520   525

Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala
    530   535   540

Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys
545   550   555   560

Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val
            565   570   575

Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu
        580   585   590

Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile
    595   600   605

Asp Thr Gly Trp
    610

<210>   58
<211>   522
<212>   PRT
<213>   Homo sapiens

<220>
<221> MISC_FEATURE
<222> (2)..(632)
<223> N- and C-terminal deleted Human ACCase1 (AAs 102-622)

<400> 58

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys
1   5   10   15

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
                20   25   30

Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu
            35   40   45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala
        50   55   60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly
65   70   75   80

Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile
                85   90   95

Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala
            100   105   110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala
        115   120   125

Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile
    130   135   140

Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp
145   150   155   160

Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys
                165   170   175

Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys
            180   185   190

Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val
        195   200   205

Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Val
    210   215   220

147

Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln Val Gln Ala Glu
225   230   235   240

Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala Lys Gln Ser Arg
            245   250   255

His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser
            260   265   270

Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile
        275   280   285

Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val Phe Glu His Met
    290   295   300

Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly Tyr Val Ser Ala
305   310   315   320

Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe Tyr Phe Leu
            325   330   335

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Val
        340   345   350

Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile
        355   360   365

Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr Gly Val Ser Pro
    370   375   380

Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala His Val Pro Cys
385   390   395   400

Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp
            405   410   415

Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg
            420   425   430

Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Ala Gly Gly
        435   440   445

Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly
    450   455   460

148

```
Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu
465                 470                 475                 480


Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
                485                 490                 495


Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp
                500                 505                 510


Leu Asp Arg Leu Ile Ala Glu Lys Val Gln
            515                 520


<210>  59
<211>  512
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<222>  (2)..(512)
<223>  N- and C-terminal deleted Human ACCase1 BC domain (AAs 102-512)


<400>  59

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys
1               5                   10                  15


Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
            20                  25                  30


Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu
            35                  40                  45


Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala
        50                  55                  60


Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly
65                  70                  75                  80


Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile
                85                  90                  95


Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala
            100                 105                 110


Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala
            115                 120                 125


                                149
```

Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile
    130   135   140

Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp
145   150   155   160

Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys
                165   170   175

Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys
            180   185   190

Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val
            195   200   205

Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys Val
    210   215   220

Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln Val Gln Ala Glu
225   230   235   240

Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala Lys Gln Ser Arg
                245   250   255

His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser
            260   265   270

Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile
        275   280   285

Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val Phe Glu His Met
    290   295   300

Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly Tyr Val Ser Ala
305   310   315   320

Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe Tyr Phe Leu
            325   330   335

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Val
            340   345   350

Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile
        355   360   365

150

Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr Gly Val Ser Pro
    370   375   380

Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala His Val Pro Cys
385   390   395   400

Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp
            405   410   415

Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg
            420   425   430

Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Ala Gly Gly
        435   440   445

Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly
    450   455   460

Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu
465   470   475   480

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
            485   490   495

Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp
            500   505   510

<210> 60
<211> 764
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(764)
<223> C-terminal deleted Human ACCase2 BC domain (AAs 1-764)

<400> 60

Met Val Leu Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr
1   5   10   15

Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile
            20   25   30

Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe
        35   40   45

```
Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly
    50                  55                  60

His Thr Leu Pro Lys Thr Pro Ser Gln Ala Glu Pro Ala Ser His Lys
65                  70                  75                  80

Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His
                85                  90                  95

Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser
                100                 105                 110

Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr
        115                 120                 125

Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala
    130                 135                 140

Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln
145                 150                 155                 160

Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp
                165                 170                 175

Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser
                180                 185                 190

Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly
        195                 200                 205

Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu
    210                 215                 220

His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg
225                 230                 235                 240

Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly
                245                 250                 255

Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala
                260                 265                 270

Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg
        275                 280                 285

Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu
```

152

Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val
305   310   315   320

Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val
                325   330   335

Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly
            340   345   350

His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly
            355   360   365

Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp
            370   375   380

Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu
385   390   395   400

Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu
                405   410   415

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly
            420   425   430

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly
            435   440   445

Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
450   455   460

Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val
465   470   475   480

Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln
                485   490   495

His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn
            500   505   510

Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln
            515   520   525

Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe
            530   535   540

```
Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr
545             550             555             560

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe
            565             570             575

His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr
            580             585             590

Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala
            595             600             605

Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly
    610             615             620

Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn
625             630             635             640

Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu
            645             650             655

Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu
            660             665             670

Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala
            675             680             685

Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe
    690             695             700

Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala
705             710             715             720

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr
            725             730             735

Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp
            740             745             750

Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val
    755             760

<210> 61
<211> 754
<212> PRT
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154

<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(754)
<223> C-terminal deleted Human ACCase2 BC domain (AAs 1-754)

<400> 61

Met Val Leu Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr
1   5   10   15

Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile
            20   25   30

Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe
        35   40   45

Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly
    50   55   60

His Thr Leu Pro Lys Thr Pro Ser Gln Ala Glu Pro Ala Ser His Lys
65   70   75   80

Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His
                85   90   95

Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser
                100   105   110

Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr
            115   120   125

Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala
    130   135   140

Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln
145   150   155   160

Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp
                165   170   175

Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser
                180   185   190

Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly
        195   200   205

155

Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu
210   215   220

His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg
225   230   235   240

Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly
            245   250   255

Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala
            260   265   270

Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg
            275   280   285

Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu
    290   295   300

Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val
305   310   315   320

Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val
            325   330   335

Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly
            340   345   350

His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly
            355   360   365

Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp
    370   375   380

Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu
385   390   395   400

Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu
            405   410   415

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly
            420   425   430

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly
    435   440   445

156

Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile
    450   455   460

Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val
465   470   475   480

Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln
                485   490   495

His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn
            500   505   510

Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln
            515   520   525

Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe
    530   535   540

Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr
545   550   555   560

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe
            565   570   575

His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr
            580   585   590

Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala
            595   600   605

Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly
    610   615   620

Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn
625   630   635   640

Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu
            645   650   655

Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu
            660   665   670

Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala
            675   680   685

Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe

Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala
705   710   715   720

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr
                    725   730   735

Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp
                740   745   750

Thr Gly

<210> 62
<211> 522
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (2)..(522)
<223> N- and C-terminal Human ACCase2 BC domain (AAs 224-764)

<400> 62

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg
1   5   10   15

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
            20   25   30

Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu
            35   40   45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala
        50   55   60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly
65   70   75   80

Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile
                85   90   95

Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala
            100   105   110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala

158

Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile
        130   135   140

Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg
145   150   155   160

Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln
                165   170   175

Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val
                180   185   190

Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly Phe Pro
                195   200   205

Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys
        210   215   220

Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser
225   230   235   240

Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala
                245   250   255

Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val
                260   265   270

Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile
        275   280   285

Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe
        290   295   300

Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser
305   310   315   320

Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe
                325   330   335

Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met
                340   345   350

Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly
        355   360   365

Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser
    370   375   380

Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro
385   390   395   400

Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro
            405   410   415

Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe
            420   425   430

Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly
        435   440   445

Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp
    450   455   460

Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys
465   470   475   480

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile
            485   490   495

Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly
            500   505   510

Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val
        515   520

<210> 63
<211> 512
<212> PRT
<213> Homo sapiens

<220>
<221> MIC_FEATURE
<222> (2)..(512)
<223> N- and C-terminal deleted Human ACCase2 BC domain (AAs 224-754)

<400> 63

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg
1   5   10   15

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
            20   25   30

Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu
        35   40   45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala
        50   55   60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly
65   70   75   80

Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile
                85   90   95

Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala
            100   105   110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala
            115   120   125

Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile
    130   135   140

Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg
145   150   155   160

Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln
                165   170   175

Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val
            180   185   190

Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly Phe Pro
        195   200   205

Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys
    210   215   220

Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser
225   230   235   240

Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala
            245   250   255

Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val
            260   265   270

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Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile
    275   280   285

Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe
    290   295   300

Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser
305   310   315   320

Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe
                325   330   335

Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met
                340   345   350

Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly
        355   360   365

Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser
    370   375   380

Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro
385   390   395   400

Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro
                405   410   415

Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe
                420   425   430

Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly
        435   440   445

Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp
    450   455   460

Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys
465   470   475   480

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile
                485   490   495

Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly
            500   505   510

162

<210> 64
<211> 521
<212> PRT
<213> Magnaporthe grisea

<220>
<221> MISC_FEATURE
<222> (1)..(521)
<223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 72-592)

<400> 64

Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile
1   5   10   15

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala
            20   25   30

Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala
        35   40   45

Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr
    50   55   60

Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu
65   70   75   80

Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu
            85   90   95

Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile
            100   105   110

Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile
        115   120   125

Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp
    130   135   140

Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val
145   150   155   160

Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln
            165   170   175

Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys
            180   185   190

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Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Ala Val Ser Glu
        195             200             205

Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly
        210             215             220

Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu
225             230             235             240

Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu Phe Gly
            245             250             255

Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala
            260             265             270

Pro Val Thr Ile Ala Lys Pro Asp Thr Phe Lys Ala Met Glu Glu Ala
            275             280             285

Ala Val Arg Leu Gly Arg Leu Val Gly Tyr Val Ser Ala Gly Thr Val
    290             295             300

Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys Phe Tyr Phe Leu Glu Leu
305             310             315             320

Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Gly Val Ser Gly
            325             330             335

Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu
            340             345             350

His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu
            355             360             365

Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr
    370             375             380

Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr
385             390             395             400

Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His
            405             410             415

Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val
            420             425             430

Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His
```

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val
    450   455   460

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val
465   470   475   480

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr
                485   490   495

Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr Ala
                500   505   510

Glu Arg Pro Asp Lys Met Leu Ala Val
                515   520

<210> 65
<211> 511
<212> PRT
<213> Magnaporthe grisea

<220>
<221> MISC_FEATURE
<222> (1)..(511)
<223> N- and C-terminal deleted Magnaporthe ACCase BC domain (AAs
      72-582)

<400> 65

Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile
1   5   10   15

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala
                20   25   30

Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala
                35   40   45

Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr
    50   55   60

Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu
65   70   75   80

Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu
                85   90   95

Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile
            100   105   110

Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile
            115   120   125

Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp
    130   135   140

Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val
145   150   155   160

Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln
                165   170   175

Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys
            180   185   190

Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Ala Val Ser Glu
            195   200   205

Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly
    210   215   220

Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu
225   230   235   240

Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu Phe Gly
                245   250   255

Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala
            260   265   270

Pro Val Thr Ile Ala Lys Pro Asp Thr Phe Lys Ala Met Glu Glu Ala
            275   280   285

Ala Val Arg Leu Gly Arg Leu Val Gly Tyr Val Ser Ala Gly Thr Val
    290   295   300

Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys Phe Tyr Phe Leu Glu Leu
305   310   315   320

Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Gly Val Ser Gly
                325   330   335

Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu

166

His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu
     355   360   365

Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr
     370   375   380

Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr
385   390   395   400

Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His
           405   410   415

Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val
          420   425   430

Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His
      435   440   445

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val
     450   455   460

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val
465   470   475   480

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr
          485   490   495

Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr
      500   505   510

<210> 66
<211> 501
<212> PRT
<213> Magnaporthe grisea

<220>
<221> misc_feature
<223> N- and C-terminal deleted Magnaporthe ACCase BC domain (AAs 72-572)

<400> 66

Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile
1   5   10   15

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala

Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala
      35   40   45

Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr
      50   55   60

Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu
65   70   75   80

Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu
            85   90   95

Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile
            100   105   110

Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile
          115   120   125

Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp
     130   135   140

Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val
145   150   155   160

Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln
            165   170   175

Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys
          180   185   190

Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Ala Val Ser Glu
          195   200   205

Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly
          210   215   220

Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu
225   230   235   240

Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu Phe Gly
            245   250   255

Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala
          260   265   270

Pro Val Thr Ile Ala Lys Pro Asp Thr Phe Lys Ala Met Glu Glu Ala
        275   280   285

Ala Val Arg Leu Gly Arg Leu Val Gly Tyr Val Ser Ala Gly Thr Val
        290   295   300

Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys Phe Tyr Phe Leu Glu Leu
305   310   315   320

Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Gly Val Ser Gly
                325   330   335

Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu
                340   345   350

His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu
        355   360   365

Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr
        370   375   380

Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr
385   390   395   400

Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His
                405   410   415

Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val
                420   425   430

Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His
        435   440   445

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val
        450   455   460

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val
465   470   475   480

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr
                485   490   495

Ile Thr Thr Gly Trp
                500

<210> 67
<211> 491
<212> PRT
<213> Magnaporthe grisea

<220>
<221> MISC_FEATURE
<222> (1)..(491)
<223> N- and C-terminal deleted ACCase BC domain (AAs 72-562)

<400> 67

Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile
1   5   10   15

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala
            20   25   30

Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala
        35   40   45

Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr
    50   55   60

Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu
65   70   75   80

Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu
                85   90   95

Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile
                100   105   110

Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile
            115   120   125

Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp
    130   135   140

Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val
145   150   155   160

Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln
                165   170   175

Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys
            180   185   190

Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Ala Val Ser Glu
    195   200   205

Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly
    210   215   220

Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu
225   230   235   240

Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu Phe Gly
          245   250   255

Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala
          260   265   270

Pro Val Thr Ile Ala Lys Pro Asp Thr Phe Lys Ala Met Glu Glu Ala
          275   280   285

Ala Val Arg Leu Gly Arg Leu Val Gly Tyr Val Ser Ala Gly Thr Val
       290   295   300

Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys Phe Tyr Phe Leu Glu Leu
305   310   315   320

Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Gly Val Ser Gly
          325   330   335

Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu
          340   345   350

His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu
          355   360   365

Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr
          370   375   380

Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr
385   390   395   400

Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His
          405   410   415

Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val
          420   425   430

Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His
        435   440   445

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val
    450   455   460

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val
465   470   475   480

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala
            485   490

<210> 68
<211> 525
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(525)
<223> N-terminal deleted Yeast ACCase BC domain (AAs--57-581)

<400> 68

Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val
1   5   10   15

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp
            20   25   30

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu
            35   40   45

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro
    50   55   60

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp
65   70   75   80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His
                85   90   95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg
            100   105   110

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly
        115   120   125

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```
Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys
    130                 135                 140

Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys
145                 150                 155                 160

Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys
                165                 170                 175

Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro
                180                 185                 190

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Gln
            195                 200                 205

Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn
    210                 215                 220

Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala
225                 230                 235                 240

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile
            245                 250                 255

Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile
            260                 265                 270

Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu
    275                 280                 285

Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser
    290                 295                 300

Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr
305                 310                 315                 320

Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu
                325                 330                 335

Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met
            340                 345                 350

Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met
            355                 360                 365

Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp
```

Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala
385   390   395   400

Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly
            405   410   415

Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly
            420   425   430

Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser
            435   440   445

Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg
            450   455   460

Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe
465   470   475   480

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe
            485   490   495

Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His
            500   505   510

Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val
            515   520   525

<210> 69
<211> 515
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(515)
<223> N- and C-terminal deleted Yeast ACCase BC domain (AAs 57-571)

<400> 69

Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val
1   5   10   15

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp
            20   25   30

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro
    50   55   60

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp
65   70   75   80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His
                85   90   95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg
                100   105   110

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly
                115   120   125

Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys
    130   135   140

Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys
145   150   155   160

Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys
                165   170   175

Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro
                180   185   190

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Gln
                195   200   205

Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn
    210   215   220

Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala
225   230   235   240

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile
                245   250   255

Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile
                260   265   270

Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu
    275   280   285

Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser
290   295   300

Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr
305   310   315   320

Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu
                325   330   335

Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met
            340   345   350

Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met
            355   360   365

Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp
    370   375   380

Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala
385   390   395   400

Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly
                405   410   415

Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly
            420   425   430

Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser
            435   440   445

Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg
    450   455   460

Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe
465   470   475   480

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe
                485   490   495

Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His
            500   505   510

Lys Met Thr
    515

176

<210> 70
<211> 505
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(505)
<223> N- and C-terminal deleted Yeast ACCase BC domain (AAs 57-561)

<400> 70

Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val
1   5   10   15

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp
                20   25   30

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu
            35   40   45

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro
        50   55   60

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp
65   70   75   80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His
                85   90   95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg
                100   105   110

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly
                115   120   125

Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys
        130   135   140

Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys
145   150   155   160

Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys
                165   170   175

Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro
                180   185   190

177

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Gln
        195   200   205

Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn
        210   215   220

Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala
225   230   235   240

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile
            245   250   255

Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile
        260   265   270

Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu
        275   280   285

Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser
    290   295   300

Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr
305   310   315   320

Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu
            325   330   335

Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met
            340   345   350

Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met
        355   360   365

Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp
    370   375   380

Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala
385   390   395   400

Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly
            405   410   415

Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly
        420   425   430

Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser
        435   440   445

Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg
        450   455   460

Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe
465   470   475   480

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe
                485   490   495

Glu Asp Asn Thr Ile Thr Thr Gly Trp
            500   505

<210> 71
<211> 495
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MISC_FEATURE
<222> (1)..(495)
<223> N- and C-terminal deleted YEast ACCase BC domain (AAs 57-551)

<400> 71

Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val
1   5   10   15

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp
            20   25   30

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu
            35   40   45

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro
        50   55   60

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp
65   70   75   80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His
            85   90   95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg
            100   105   110

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly
        115   120   125

Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys
        130   135   140

Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys
145   150   155   160

Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys
            165   170   175

Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro
        180   185   190

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Gln
        195   200   205

Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn
        210   215   220

Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala
225   230   235   240

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile
            245   250   255

Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile
            260   265   270

Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu
        275   280   285

Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser
        290   295   300

Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr
305   310   315   320

Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu
            325   330   335

Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met
            340   345   350

Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met

Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp
    370   375   380

Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala
385   390   395   400

Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly
                405   410   415

Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly
            420   425   430

Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser
        435   440   445

Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg
    450   455   460

Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe
465   470   475   480

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp
                485   490   495